

## FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCTCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACGCGTCCGGGCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTCGCTCTCCCG  
CAGCGCTACCCGCCATGCGCTGCCGCGCCGGCCGCGCTGGGGCTCCTGCCGCTCTCTGCTG  
CTGTGCCGCCCGCGCCGAGGCGCCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT  
GGTGGACAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATC  
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA  
GGCGCAGGGTCTCTGCCGTCGCCACATGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT  
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG  
CGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGTGAGGAAAAACG  
AAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTCTCTGACGGCTTCGAAGAAACG  
GAAGATGCCTGTGTGCCGCCGCGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT  
GCCCTCCCGCGAAGACCTGTAATGTGCCGGAATTACCTTTAAATTATTTCAGAAGGATGTCC  
CGTGGAATAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTCTTGGTTGTTCTTA  
AACAGACTTGATATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC  
TTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA  
TCACAAATTTACAAATAAAGCATTTTTTCTACTGCATTCTAGTTGTGGTTTGTCCAAACTC  
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAACTCGGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACCTTGGTTAGGTACCTTCTGAGGCGGAAAGAACAGCTGTGGAATG  
TGTGTCAAGTTAGGGTGTGGAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop  
><MW: 38192, pI: 4.53, NX(S/T): 2  
MRLFRRAALGLLPLLLLLPPAPEAAKKPTFCHRCRGLVDKFNQGMVDATAKNGFGGNTAWEETLSKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWLQLKSEYDPLFEWFCVKTLKVVCCSPGTGPDCLACQGGQRPCSG  
NGHCSGDGSRQGDGSCRCHMGYQGFLCTDCMDGYFSSLRNETHSICTACDESKTCSGLTNRDCGCEVGVWLDE  
GACVDVDECAAEPPPCSAQFCKNANGSYTCEEDSSCVGCTGEGFGNCKECISGYAREHGQCADVDECSLAKE  
CVRKNENYNTPGSYVVCVCPDGFEEEDACVPPAAEAATEGESPTQLPSREDL

### **Signal peptide:**

amino acids 1-24

### **N-glycosylation sites.**

amino acids 190-194 and 251-255

### **Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

### **Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

### **Tyrosine kinase phosphorylation site.**

amino acids 303-310

### **N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

### **EGF-like domain cysteine pattern signature.**

amino acids 166-178

### **Leucine zipper pattern.**

amino acids 94-116

## FIGURE 3

CAGGTCCAATGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGCGCCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTTTCCCGGCAGCGAGGAGTCTGAGCAGCATGGCCCGGAGGAGCGCCTTC  
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC  
CGGGCCGCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA  
TAGGATTTGAAGAAGATATCCTGATTGTTTCAGAGGGGAAAAATGGACCTTTTACATATGAT  
TTCAGAAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAAATATCCATTCCATGAATTTTAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCTCTTGGCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA  
TCAGTTGTTTCAAGTTGGTTTCCCATGTCTTGAAAAACAGGATGGGGTGGCAGCATTTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCCAACACCTCAAATGCTATCT  
TCTTTAAACATGTCAACAAGCTGAGTGCCAGGCGGGTGCCGAATGGAGGCTTTTGTAAAT  
GAAAGACGCATCTGCGAGTGCTCTGATGGGTCCACGGACCTCACTGTGAGAAAGCCCTTG  
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG  
GATTTCTATGGAGTGAACCTGTGACAAAGCAAACCTGCTCAACCACTGCTTTAATGGAGGGACC  
TGTTTCTACCTGGAAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAAATGCCCACAACCTGTGCAAAATGGAGGTAAATGCATTGGTAAAGCAAAATGTAAGTGTT  
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGACAT  
GGAACCTGCCATGAACCAACAATGCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAGGTACGAAGCCAGCCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC  
ACAGCCTTCACTTAAAAAGGCCGAGGAGCGCGGGATCCAATGAATCCAATTACATCTGG  
TGAACCTCCGACATCTGAACGTTTAAAGTTACACCAAGTTTATAGCCTTTGTTAACCTTTCA  
TGTGTTGAATGTTCAAAATAATGTTTATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT  
TCAATTATAAATCACTGAGCTGATATTTACTCTTCTTTTAAAGTTTCTAAGTACGCTGTAG  
CATGATGGTATAGATTTTCTTGTTCAGTGCTTTGGGACAGATTTTATATATGTCAATTGA  
TCAGGTTAAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAAATTACAATGCATTTATGGT  
GTCTGGGGGCGAGGGAAACATCAGAAAGGTTAAATTTGGGCAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTGCAATTAAATGTTGAAGTTACAGCATTTCAGATTTTATTGTGATATTTAGAT  
GTTTGTGTACATTTTAAAAAATTGCTCTTAATTTTAAACTCTCAATACAATATATTTTGACC  
TTACCATTATTCAGAGATTCAAGTATAAAAAATAAATTAACACTGTGGTAGTGGCATT  
TAAACAATATAATATATTTCAACACAATGAATAGGGAATATAATGTATGAACCTTTTGCAT  
TGCTTGAAGCAATATAATATATTTGTAACAAAACACAGCTCTTACCTAATAAACATTTTAT  
ACTGTTTGTATGTATAAAATAAGGTGCTGCTTTAGTTTTTTGGAAAAAATAAATAAATAA  
AAAAAATAAATAAATAAATAAAGGCGCGGCTAGAGTGCACCTGCAGAAGCTTGGC  
CGCCATGGCCCACTTGTTTATTGAGCTTATAATG

## **FIGURE 4**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC
RNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFICPPGFGVNC DKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCI GSKCKSKGYQGDLC SKPVC
EPGCGAHGTCHPENKQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
```

### **Signal peptide:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 88-92, 245-249

### **Casein kinase II phosphorylation site.**

amino acids 319-323

### **Tyrosine kinase phosphorylation site.**

amino acids 370-378

### **N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

### **ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

### **EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGAGGCGCGGGCCAGCCTGGG  
CCCCAGCCCCACACCTTCACCAGGGGCCAGGAGCCACCATGTTGGCGATGTCCACTGGGGCTAC  
TGCTGTTGCTGCCCGTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCTGGGCGCCGG  
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCCGGGCGGTGCCGACGACTGTGCCCTGCCCCCTACCTGGGCGCCATCT  
GTTACTGTGACCTCTTCTGCAAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCCTGGCGTGGCACCCCTTTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA  
TCCAGTCTTGGGAACGTACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAAACACAGCGCCTTCTGGGGCATGACCTGGATGAAGGGCATTTCGCTACCGCCTGGGCACCA  
TCCGCCCATCTTCTCGGTCAAGAACATGCATGAAATTTATACAGTGCTGAACCCAGGGGAG  
GTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACTGATTATGAGCCTCTTGA  
CCAAGGCAACTGTGCAGGCTCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCCCCAGAACCTGCTGTCTTGTGAC  
ACCCACAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTCTCTGCGTCTG  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGGCAAGCGCCAGGCCACTGCC  
GACTGCCCCAACGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTTCTTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCTGGGGCC  
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGGCGGGCGTCAATGAGTGCGACATCGAG  
AGCTTCTGCTGTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCTACTGAGGCTG  
CGGGCACCACGCGGGGTCCGGCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG  
GGGCGGTGACCCAGCCTCGCCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT  
CGCGGCGCGGGTTCCGCTGACGCGAGCGCCCCGCTGGGAGCCGCGGGCAGGCAGACTGGCG  
GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCTGGGAAGAGCACAGCTGACG  
ATCCCAGGCCTCTGGGCGCCCCACTCAAGACTACCAAAGCCAGGACCTCAAGTCTCCAGC  
GCCAATACCCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTATAGACAGGGTCTTGCTCCG  
TTGCCAGGTTGGAGTGAGTGGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTC  
AGTGACCTCCCACTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCAACCACTGGC  
TAATTTTGTATTTTGTAAAGAGGGGGTCTCACTGTGTTGCCCAGGCTGTTTCGAACT  
CTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGTGGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTCTCAGATATTATTTTCTTTTTCATCTGTTTTAAAA  
TAAACCAAAGTATTGATAAAAAAAA

## **FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPGLGLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQDLCCRGRADDC
ALPYLGAIICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
```

### **N-glycosylation site.**

amino acids 78-82, 161-165

### **Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

### **N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

### **Amidation site.**

amino acids 26-30, 318-322

### **Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCCTTGCCCTTTTTCACAGCAAGCTTNTGCNATCCCGATTGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCTGTCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC  
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCCTGGTGGTTCTGCGTCGCCGAGG  
GNTGGTGTCTGACCCTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGGTCGGGGCAAGCGCCAGGCCACTGCCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG  
TGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATACCGCCGCATGGGACCCACTCAG

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## FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAAGCTGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCTGCTGCTCTGGGGACCCGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGTGGGAGCCTGTCCTGGTTCCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCACCCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCCTGCAGATGGCCCTCCAACCTCTCTGCTGCTGTTTC  
CATGGCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCAGGAAGCCTT  
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTTCCTGGGAGTCTCCAGAGATGGGGCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTCTGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAAA



## **FIGURE 9**

MTHRTTTWARTSRAVTPTCATPAGPMPCSRLLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPFPMALSRTPTTRQISSDT  
DPPADGFSNPLCCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

### **Signal peptide:**

amino acids 1-47

### **N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

### **N-myristoylation site.**

amino acids 56-60

### **Amidation site.**

amino acids 70-74

## FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCTGCTGCCCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAAGTACCCGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC  
TCATAGTGGAGACGGACACGTTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGAAGAGCAAAGACTG  
CGTGTTCACGGAGATCGTGCTGGAGAACAACTATACGGCCTTCAGAACGCCCGGCACGAGG  
GCTGGTTCATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC  
CAGCGCGAGGCCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCAGC  
CAGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGACCAAGCGCACAC  
GGCGGCCCCAGCCCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCCGCCTCCC  
CACCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC  
GAGGGAGGACCTGAGGGCCGCGAAGCATCCGAGCCCCAGCTGGGAAGGGGCAGGCCGGTG  
GCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGACGGGTGGCAGGCCCTGGAGAGGAACT  
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCTCCAGCCGGGCTCCTGAAGCC  
GCTGAAAGGTACGCGACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCTCAAAA  
CTGTCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCCAAACCTCCTCTGGCTAGACTGTA  
GGAAGGACTTTTGTGTTGTTGTTGTTTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAAATAG  
AGGGTTGTCCACTCCTCACATTCCAGACCCAGGCCTGCACCCACCCCCCACTCCAGCCC  
CGGAATAAAACCATTTTCTGTC

## **FIGURE 11**

MGAARLLPNLTLCLQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGLIGKPSGKSKDCVFTEIVLENNYTAFAQNARHEGWFMATFRQGRPRQASRSRQNRQREAHFIKRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

### **Signal peptide:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 9-13, 126-130

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

### **Casein kinase II phosphorylation site.**

amino acids 65-69

### **Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

### **N-myristoylation site.**

amino acids 69-75, 188-194

### **Amidation site.**

amino acids 58-62

### **HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTGTGCATGGAG  
GACAGCAGCAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT  
CATTTTGATTTTGCTGTTTATTTTCTTTTCTTTTCTTTTCCACCACATTGTATTTTAT  
TTCCGTACTTCAGAAATGGGGCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTCTCT  
GAAGCTCTGGCTTATCATTTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCGTCC  
CTAGTGTGTGCCCGTGCACAGGAACCTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG  
CCTCTTGGGATCCCGAGGGCGTAACCGTACTCTACCTCCACAAACCAAATTAATAATGC  
TGGATTTCCTGCAGAACTGCACAAATGTACAGTCCGGTGCACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTTCCCATGAACCTTCCCAGAATGTGAGAGTTCTCCATTGCGAGGAAAAAC  
AATATTCAGACCATTTTACGGGCTGCTCTTGGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAAATCGAATTGCTGTTCATATCCGACATGGCCCTCCAGAA  
TCTCAGAGCTTGGAGCGCTCTTATTGTGACGGGAACCTCCTGACCAACAAAGGTATCGCCG  
AGGGCACTT CAGCCATCTCCCAAGCTCAAGGAATTTCAATTGTACGTAATTTCGCTGTCC  
CACCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGTGAGGACAACCAGAT  
TAAACCATTTCCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACTGAAGCAGCTC  
ACTGCTCGGAATAACCCCTTGGTTTTGTGACTGCAAGTATTAATGGGTACAGAATGGGTCAA  
ATATATCCCTTCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTGAAACAGTCCGGG  
GGATGGCCCTCAGGGAATTAATATGAATCTTTTGTCTGTCCACCACGACCCCGGGCTGT  
GCTCTCTTACCACCAGCCCAAGTACAGCTTCTCCGACCACCTCAGCCTCCACCCCTCTCTAT  
TCCAAACCTTAGCAGAAGCTACACGCCTCCAACTCCTACACATCGAAACTTCCACGATTC  
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTCTGAAACGGATCCAGCTCTCTATC  
CATTTTGTGAATGATACTTCATTCAGTCAAGTCAAGTGGCTCTCTCTCTTACCGTGATGGCATA  
CAAACTCACATGGGTGAAAAATGGGCCACAGTTTAGTAGGGGGCATGTTT CAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTTAGTGCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTT CAGAGGC  
CACCACCCATGCCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
EGTCCCACAGCATGGGCTCCCCCTTCTGTCTGGCGGGCTTGATCGGGGGCGCGGTGATATT  
GTGCTGGTGGTCTTTCTCAGCGTCTTTTGCTGGCATATGCACAAAAAGGGGCGCTACACCTC  
CCAGAAGTGAAATACAACCGGGGCGGGCGGAAAGATGATTATTGCGAGGCGAGGCACCAAGA  
AGGACAACTCCATCTGGAGATGACAGAAACAGTTTTCAGATCGTCTCTTAAATAACAGAT  
CAACTCCTTAAAGGAGATTTCAGACTGCAGCCCATTTACACCCCAATGGGGGCATTAAATTA  
CAGAGACTGCCATATCCCCAACAACTGCGATACCTGCAACAGACAGCTGCCAGACCTGGAGC  
ACTGCCATACGTGACGAGCCAGAGGCGGCTTATCAAGCGGACAACTAGACTTTGAGAA  
CACACTCGTGTGTGCACATAAAGACAGCAGATTACATTGTATAAATGTTACACAGATGCAT  
TTGTGCAATTTGAAATCTCTGTAATTTATACGGTGTACTATATAATGGGATTAAAAAAGTG  
CTATCTTTCTATTTCAGGTTAATTACAAACAGTTTGTAACTCTTTGCTTTTAAATCTT

## FIGURE 13

MGLQTTKWP SHGAFFLKSWLIISGLYSQVSKLLACPSVCRCDNFVYCNERSLTSVPLGIP  
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKEELHDDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN  
PWFCDCSIKWTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELNMNLLSCPTTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGREVRTPPISERIQLSIHFVND  
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNRYAVEDTICSEATHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQKWKYNRRKKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVDPDLEHCHT

### Signal peptide:

amino acids 1-42

### Transmembrane domain:

amino acids 542-561

### N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

### Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

### Tyrosine kinase phosphorylation site.

amino acids 319-328

### N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

### Amidation site.

amino acids 581-585

### Leucine zipper pattern.

amino acids 164-186

### Phospholipase A2 aspartic acid active site.

amino acids 39-50

## FIGURE 14

ACTTGGAGCAAGCGGCGCGGAGACAGAGGCGAGAGGCAGAAGCTGCGGCTCCGCTCTCCACGAGCG  
 ATCCCCGAGAGAGCCGCGGCCCTCTGGCGAGCGGAAGAGCCGACGAGGAGACCCGAGTGGCTGCGCCCTGCC  
 TCGCTTCCCGAGCGCGCGGCTGCGAGCCTTGCCCTCTTGCTCGCCTTGAAAATGAGAAAGATGCTCGCAGGCT  
 GCTTTCTGCTGATCTCGGACAGATCGTCTCTCTCTGCCGAGGCGCAGGAGCGGTGACGTGGAGGTCTTCATCT  
 CTAGGGGCGACACACGCTCGGACCCGACCCGCGAGCGGCCCTCTGGAGAGTTCCTGTGAGAACAGCGGGCGAGCC  
 TGGTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAAGGTCAAGGAGTTCATCGTGGACA  
 TCTTGCAATTCTTGACATTGGTCCGTGATGTCACCGAGTGGCGCTGCTCCAAATGCGAGCACTGTCAAGAAATG  
 AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGG  
 GCACCATGACTCGGCTGCCATCCAGATGTGCCCTGAACATCGCATTTCTCAGAAAGCAGAGGGGGCCCGGCCCTGA  
 GGGAGAAATGTGCCACGGGTATATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTCGCGCAGGTGGCTGCTA  
 AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCGCAGGTAGACTTCAACACCTTGAAGTCCATTG  
 GGAAGTGAGCCCATGAGGACCATGTCTCTGTGTGCCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
 AGAAGAAGTTGTGCACGGCCCATCATGTGACGACCCCTGGAGCATAACTGTGCCACTTCTGCATCAACATCCCTG  
 GCTCATACGCTGCGAGGTGCAAAACAGGCTACATTTCAACTCGGATCAGACGACTTGCAAGATCCAGGATCTGT  
 GTGCCATGGAGGACCACAACGTGAGCAGCTCTGTGTGAATGTGCGGGCTCCTTCGTCTGCCAGTGCTACAGTG  
 GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAAACCCAGGATGTGAAC  
 ATGAGTGTGTAAATGCTGATGGTCTCTACCTTTGCCAGTCCATGAAGGATTTGCTCTTAACCCAGATGAAAAA  
 CGTGCACAAGGATCAACTACTGTGCTACTGAACAAACCGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT  
 ACTACTGCCCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAACTTGACGCGAGTGAGCCACTGTGTGCAC  
 AGCAGGACCATGGCTGTGAGCAGCTGTGTGTAACACGGAGGATTCCTTCGTCTGCCAGTGCTCAGAAAGGCTCC  
 TCACTAAGCAGGACCTCAAGACCTGTCTCCGGGTGGATTACTGCCCTGCTGAGTGACCATGGTTGTGAATACTCT  
 GTGTCAACTGGACAGATCTTTGCCCTGTGAGTCTCTGAGGACAGCTGCTCCGACGATGGGAAGACGCTGTG  
 CAAAATTGGACTCTTGCTCTGCGGGACACGCGTGTGTAACATTCGTGTGTAAGCAGTGAAGATTCTGTTTGTGT  
 GCCAGTGGCTTGAAGTTATATACCTCCGTGAAGATGGAAAAACCTGCAGAAAGGAAGATGCTTGCCCAAGCTATAG  
 ACCATGCTTGTGAACAATTGTGTGTGAACAGTGACGACTCATACAGCTGCGAGTCTTGGAGGGATTCCSGCTG  
 GTGAGGATGGAAACGCTGCCAGGAAGAGGATGTCTGCAAAATCAACCCACCATGGCTGCAACAATTTGTGTTA  
 ATAAATGGGAATTCCTACTCTGCAATGCTCAGAGGGGATTGTTCTAGCTGAGGACGGAAGACGCTGCAAGATG  
 GCACTGAAGGCCCAATTCAGACTGCTGTTGTGTATCGATGATCCAGAGTCTTGAGAGAGAGAAATTTGAGGTCG  
 TGAAGCAGTTTGTCACTGGAATATAGATTCTTGACAATTTCCCCCAAGCGCGTCSAGTGGGGCTGCTCCAGT  
 ATTTCCACACAGGTTCCACACAGAGTTCACTCTGAGAAACTTCAACTCAGCCCAAGACATGAAAAAGCGTGGGCC  
 ACATGAATACATGGGAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAAGTTTATCCCAAG  
 GAGAGGGGGCGAGGCCCTTTCCACAAAGGTGCCGAGAGCCCATTTGTTTACCAGACGAGCGGCTCAGGATG  
 AGCTCTCGAGTGGGCGAGTAAAGCCAAAGGCCAATGATATCACTATGATGCTGTTGGGGTAGGAAAAAGCATTG  
 AGGAGGAACACAAAGAGATTGCTCTGAGCCCAAAACAGACATCTCTTCTAGCGCGAAGACTTCAGACAAATGG  
 ATGAGATAAGTGAAAAACTCAGAAAGGCACTCTGTGAAGCTCTAGAAGCTCCGATGGAAGACAGGACTCTCCAG  
 CAGGGGAACTGCCAAAAACGCTCAACAGCCCAACAGAAATCTGAGCAGTCAACATAAATATCCAGAGCTACTTT  
 TCTGTTCTAATTTTGCAAGTGCAACACAGATATCTGTTTGAAGAGACAATCTTTTACGCTCTACACAAAAGCTTT  
 CCCATTCAACAAAACCTTCAGGAAGCCCTTGGGAAGAAAAACAGATCAATGTCAAAATGTGAAAACTTATAATGT  
 TCCAGAACCTTGCAACGAAGAGTAAAGAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAAATGGAAGCCC  
 TGGAAAACTGCCCTGAGATACAGATGAGATTAGAAAATCGCGACACATTTGTAGTACTTGATACGCGATTCAAT  
 GAACGCACTGCAGAGCCCAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAAACATCAGTACTGA  
 GAAACCTGGTTTGGCACAGAACAAAGACAAAGATATACACTAACTTGATATAATTTATCTAGGAAAAACCTTCT  
 TCAGAAATCTAAGATGAATTTACACAGGTGAGAAATGAATAAGCTATGCAAGGTTATTTGTAAATATACTGTGGACAC  
 AACTGTCTCTGCCCTATCCCTGCTTGTGTGCAATCTCATTGTACTATACGATAAAGTTTGACACAGTCTTACTT  
 CTGTAGAACAATGGCCATAGGAAATGCTGTTTTTTGTACTGGACTTACCTTGATATGTATATGATATGATGTATG  
 CATAAAACTATAGGACATATGATCTTGTGGACAGGTGGATTTTTATACATATTAATATTTACCACTTCAG

## FIGURE 15

MEKMLAGCFLLLILGQIVLLPAEARERSRGRSISRGRHARTHPTQALLESSCENKRADLVFI  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNFSLKTFKRKSEVERAV  
KRMRLHSTGTMTGLAIQYALNIAFSEABGARPLRENVPRVIMIVTDGRPDQSVAEVAAKARD  
TGLLIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVVFQKKLCTAHMCSTLEHN  
CAHFICINIPGSSVCRCKQGYILNSDQTTTCRIQDLCAMEDHNCQELCVNVPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCCTRINYCALNKPGC  
EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGLI  
NEDLKTC SRVDYCLLDHGCYSCVNMDRSFACQCPFGHVLRSDDGKTC AKLDS CALGDHGCE  
HSCVSSSDSFVCQC FEGYILREDGKTCRRKDVCAIDHGCEHICVNDDSYTCECLEGFRLA  
EDGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID  
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNPNFSAKDMKKAVA  
HMKYMGKGSMTGLALKHMFERSFTQGBGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEEELQBIASEPTNKHLFYAEDFSTMDIEISEKLKKGICEALEDSDGRQDS  
PAGELPKTVQQPTSESPVTINIQDLLSCSNFAVQHRYLFEDNLLRSTQKLSHSTKPSGSPL  
EEKHDQCKCENLIMQNLANEVVRKLTQRLEEMTQRMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## FIGURE 16

GGAGCCGCCCTGGGTGTGACGGCTCGGCTCCCGCGCAGCTCCGGCCGTCGCGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCAGGGAGGGC  
CATGATTTCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAAACCGGTTGCAG  
GCGGTGGAGGGAGGGGAAGTGGTGCTTCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC  
ATCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGGTCAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC  
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT  
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT  
GTGGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTTCCATCCTTCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG  
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTTC  
TCTTGTAACACCGCCGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGACCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCTT  
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCCTGGTGCAT  
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAGACTGCCCACGACAGAT  
GGGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTTTCTTCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATATGATGAC  
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCCCACCTCTC  
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC  
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCCTTGGCTCCCACTCCAGTCTCCGTGT  
ATTGATATAACCTGTGAGCTGGCTTGGTTAGGTTTTACTGGGSCAGAGGATAGGGAATCTC  
TTATTAAACCTAACATGAAATATGTGTTGTTTCATTGCAAATTTAAATAAAGATACATAA  
TGTTTGATGAAAAA



## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVFFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCTRLQGVPHVGANVTLSQCSPRSKPAVQYQ  
WDRQLPSFQIFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA  
VVAGAVVGTLLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPPWPKSSDTISKNGTL  
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQIPISPIPGGVSSSGLSR  
MGAVPVMVPAQSQAQSLV

### **Signal peptide:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 245-267

### **N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

### **N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCGCTCCTAGTGGTTTTTCCACTTTG  
TTGAATTGTTCTCTACTCAAAATTGCACCAAGACACCTTGTCTCCAAATGCAAAATGTGA  
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGTACAA  
TTTGTGAAGATGATAATGAATGTGGAATTTAACTCAGTCTGTGGCGAAAATGTAAATTGC  
ACTAACACAGAAGGAAGTTATTATGTATGTGTGTACTGGCTTCAGATCCAGCAGTAACCA  
AGCAGGTTTTATCACTAATGTAGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATT  
TAGATAATGTCTGTATAGCTGCAAAATATTAAATAAACTTTAACAAAAATCAGATCCATAAAA  
GAACCTGTGGCTTTGCTACAAGAAGTCTATAGAAATCTGTGCAGATCTTTCACCAACAGA  
TATAATTACATATATAGAAAATATAGCTGAATCATCTTCAATTACTAGGTTACAAGAACACA  
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTACTGAATTTGTAAAAACCGTGAAT  
AATTTTGTTCAAAGGGATACATTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGGAAC  
ACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC  
AAAAGACCACAGAGTTTGATACAAATTCACCGGATATAGCTCTCAAAGTTTTCTTTTTTGAT  
TCATATAACATGAACATATTCTCCTCATATGAATATGGATGGAGACTACATAAATATATT  
TCCAAAGAGAAAAAGTCGATATGATTCAAATGGCAATGTGCAAGTTGCATTTTTATATATA  
AGAGTATTGGCTTCTTGTCTTATCATCTGACAACCTCTTATTGAAACCTCAAAATTTAGAT  
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAAACC  
ACCCACATTATGAACCTGAAAAAATAACATTTACATTAAGTCTCGAAAGGTACACAGTA  
GGTATAGGAGTCTATGTGCAATTTTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT  
CAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT  
GACACATTTGCAATTTTGATGTCTCTGGTCTTCCATTGGTATTAAAGATTATAATATTC  
TTACAAGGACTCACTCAACTAGGAATAATTAATTTCACTGATTTGTCTTGCATATGCATTTT  
ACCTTCTGGTTCTTTCAGTGAAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCTG  
TAGCCTTATTTCTGTCTGAACCTGTTTTTCTTGTGGGATCAATACAAAATACTAATAAGCTCT  
TCTGTTCATCATTTGCCGGAAGTCTACACTACTCTTTTGTAGCTGCTTTTGCATGGATGTGC  
ATTGAAGGCATACATCTCTATCTCATTGTTGTGGGTGTCTATACAACAAGGGATTTTTGCA  
CAAGAATTTTTATATCTTTGGCTATCAAGCCCGAGCCGTGGTGAATTTCCGCGAGCAC  
TAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCGAAAACAACTTTATT  
TGGAGTTTTATAGGACCGAGCATGCCATAATCATTCTGTTAATCTCTTGGCTTTTGGAGTCAT  
CATATACAAGTTTTTTCGTCACTGCAGGGTTGAAACCAGAAAGTTAGTTGCTTTGAGAACA  
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTTCTGTTCTTCTCGGCACCACTGGATCTTT  
GGGGTTCTCCATGTTGTGTCACGCATCAGTGGTTACAGCTTACCTCTTCCAGTGCAGCAATGC  
TTTCCAGGGGATGTTTCATTTTTTATTCCTGTGTGTTTTATCTAGAAAGATTCAAGAAGAA  
ATTACAGATTGTTCAAAAATGTCCCTGTTGTTTTGGATGTTTAAAGGTAACATAGAGAATG  
GTGGATAATTACAACATGCACAAAAATAAAAAATCCAAGCTGTGGATGACCAATGTATGGTTT  
TGACTCATCAAAATTATCCAATTATTAACCTACTAGACAAAAAGTATTTTAAATCAGTTTTTCT  
GTTTATGCTATAGGAACGTGATATAATAAGGTAATAATATGTATCATATAGATATACATGT  
TTTTCTATGTGAATAGTTCTGTCAAAAATAGTATTGCAGATTTTGGAAAGTAATTTGGTTT  
CTCAGGAGTGATATCACTGCACCCAGGAAAGATTTTCTTTCAACACGGAAGTATATGAA  
TGTCTGAAGGAAACCACTGGCTTGATATTCTCTGTGACTCGTGTGCTTTGAACTAGTCC  
CCTACCACCTCGTAATGAGCTCCATTACAGAAAGTGAACATAAGAGAATGAAGGGGCAGA  
ATATCAACAGTGAAGGGAATGATAAGATGATTTTGAATGAAGTGTTTTTCTGTAGAC  
TAGCTGAGAAATTTGTGACATAAAAAATAAGAAATGAAGAAACACATTTTACCATTTTGTGAA  
TTGTTCTGAAGTAAATGTCTCACTAAAAACAACTAGACTTCTGTTTGTCTAAATCTGTTTCTT  
TTTCTAATTTCTAAAAAATAAAAAAAGGTTTACCTCCACAAATTTGAAAAAATAAAAAA  
AAAAAATAAAAAAATAAAAAAATAAAAAA

## **FIGURE 19**

MKRLPLLVVVSTLLNCSYQNTCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSIYCMCVPGFRSSSNQDRFITNDGTVCIEENVNANCHLDNVCI  
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL  
SNSTLTETFEVKTVNNVFQORDTFVWVDKLSVNHRRTHLTKLMHTVEQATLRISQSFPQKTTEFDT  
NSTDIALKVFFFDSDYNMKHIHPHMNMMDGDYINIFPKRKAAYDSNGNVAVAFLLYKSI  
SSDNFLLPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF  
WNYSPTDMNGSWSSEGCCLTYSNETHTSCRCNHLTHFAILMSSGSPSIGIKDYNILTRITQLG  
IIISLCLALCIFTFFWFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIIAGL  
LHYFFLAFAWMCEIGIHLVIVGVYINKGFLHKNFYIFGYLSPAVVVGFSALGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLVHVASVVTAYLFTVSNAPQGMFIFLFLCVLSRKIQEBYYRLFKNV  
PCCFGCLR

### **Signal peptide:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 140-145, 146-148, 149-151, 152-154, 155-157, 158-160, 161-163,  
648-664

### **N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

### **Glycosaminoglycan attachment site.**

amino acids 49-53

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

### **Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

### **Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

### **N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## FIGURE 20

TGGAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAAATATATTTCCAAAGNG  
AAAAGCCGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT  
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACCTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA  
GGAGTCTATGTGGCATTTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTTCGAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTTCACGATTGTCTTGCCATATGCATTTTTACCTTC  
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

1  
2  
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## FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGTGCGCGGTGGGGAGGAGTTCCTCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACCGCCTGGGCGGGGTACACCCGGCTGGGA  
CAAGAAGCCCGCCGCTGCTCGCCGGGCCCGGGAGGGGCTGGGGCTGGGGCCGGAGGCGG  
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TGCTTTGGGCACCTACCCGTGGGGCCCGTAAGGCCTACTATATAAGGCTGCCGGCCCGGAG  
CCGCGCGCCGCTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC  
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGACCCCCATCGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
CCACGTGCATACGGCTGGGGCGACCCCATCCGCCGTGCGGCACCTGTACACCTCCGGCCCCC  
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTGTGGACTGCGCGCGGGGC  
CAGAGCGCGCACAGTTTGTGTGGAGATCAAGGCAGTCCGTCTGCGGACCGTGGCCATCAAGGG  
CGTGACAGCGTGCGGTACTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
CAGAGGCTTTCTTCCACTCTCTATTTCCTGCCCATGCTGCCCATGGTCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGGAACTGACATGTTCTCTTCGCCCTGGAGACCGACAGCATG  
GACCCATTGGGCTTGTCAACCGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTAAGT  
GAGACCATGCCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG  
TGCTTCTACAAGAACAGTCTTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA  
GTGTACATATTAGAGTTTTCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT  
GATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCCTGGGCCCCCATCTGCTCCCTCGA  
GGTGTGTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC  
TCACTTCTCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC  
GCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG  
ACCAATTGCCCCCTCCCAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCACAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTCCCC  
GTGAGGCCAGTTCTGTATGGATGCTGTCTCTGAGAATAACTTGCTGTCCCGGTGTACCTGC  
TTCCATCTCCAGCCCCACAGCCCTCTGCCACCTCACATGCTCCCCATGGATTGGGGCCT  
CCAGGCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGGAAGCCTAGAAC  
CTTTTCCCCAGCACTTGGTTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA  
TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATATTTATGTATGTAAGTGAGGTTG  
TTTTGTATATATAAATGGAGTTTGTTTG

## **FIGURE 22**

M R S G C V V V H W I L A G L W L A V A G R P L A F S D A G P H V H Y G W G D P I R L R H L Y T S G P H G L S S C F L R I  
R A D G V V D C A R G Q S A H S L L E I K A V A L R T V A I K G V H S V R Y L C M G A D G K M Q G L L Q Y S E E D C A F E E  
E I R P D G Y N V Y R S E K H R L P V S L S S A K Q R Q L Y K N R G F L P L S H F L P M L P M V P E E P E D L R G H L E S D  
M F S S P L E T D S M D P F G L V T G L E A V R S P S F E K

### **Signal peptide:**

amino acids 1-22

### **Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

### **N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCTCGACCTCCTCA  
GAGCAGCCGGTGCCTCCCCGGGAAGATGCGGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTGCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA  
AGAAGACTGTTTCTCCAGATTAGAGTGGAAGAACTGGGTCGGAGTGTCTCCTTTGTCTAC  
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG  
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCATCTG  
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGCTCCAGCAGTT  
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAAGGATGGCATCCGTTTGCTAGAAA  
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACCAATGAATACAAAACCTGGAATC  
TGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC  
TGTGGATATCGCAGGTGTCTGGGAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA  
TCATAGCAGCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA  
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCAGCCTGTAATCCAGCAGCTTTGGAAGG  
CGCGCGCGGGCGGATCACGAGGTGAGGAGTTCTAGACCAAGTCTGGCCAATATGGTGAAACCC  
CATCTCTACTAAAATACAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAAATAAA  
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

## **FIGURE 24**

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRL  
WKKLGRSVSFVYYQQTQGDFFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED  
TVTLEVLVAPAVPSCVFPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST  
NSSYTMNTKTGTQLQNTVSKLDTGEYSCEARNVSGYRRCPCGKRMQVDDLNISGIIAAVVVVA  
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTVPVLPALWKAAGGSRGQEF

### **Signal peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 130-144, 238-258

### **N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

### **Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

### **N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

### **Amidation site.**

amino acids 226-230



## FIGURE 25

GACATCGGAGGTTGGGCTAGCACTGAACTGCCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCTGGCAT  
CATGCTGCTATTTCCTGCAAACTACTGAAGAAGCATGGGATTTAAATATTTTACTTCTTAAATAA  
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA  
TTATATCATTAAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTGGACAATG  
CAATTGTGGCACTGGCATTATTTCAGTGAAGAAAAAATCTTGTGGTTCTATGGCATTATCA  
TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACCTTACTAGCACTGACTG  
TGGAACTCCTTAAAGGGCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGCTTTTAACTTTCCAGCCAGATTGCC  
AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAG  
ACTTTCAGTAAACCTTACTGGCCTGGGATTATCTCAAAACAATTTATCTTCAGTCACCAAT  
ATTAATGTAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAACTTACTGA  
ACTGCCTGAAAAATGTCTGTCCGAACCTGAGCAACTTACAGAACCTCTATATTAATCACAACT  
TGCTTTCTCAATTTTCAAGTGGAGCCTTTATTGGCTACATAATCTTCTTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAATCTAGAGAT  
TCTGATGATTGGGGAAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAAGCCTCTTATCA  
ATCTTCCGACGCTGGTTTATAGCTGGTATAAACTCACAGAAATACCAGATAACGCCTTGGTT  
GGACTGGAAAACTTAGAAGCATCTCTTTTTACGATAACAGGCTTATTAAGTACCCCATGT  
TGCTCTTCAAAAAGTTGTAAATCTCAAATTTTGGATCTAAATAAAATCCTATTAAATAGAA  
TACGAAGGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAAATAATATGCCT  
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC  
TACTAACACCCCTAGATTGTCTTACATTCACCCCAATGCATTTTTCAGCTCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCATTGAGTCTCTG  
CCAAACCTCAAGGAAATCAGCATACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTG  
GATGAACATGAACAAAAACCAACATTCGATTTCATGGAGCCAGATTCACTGTTTTGCGTGGACC  
CACCTGAATTCGAAGTCAAGATGTTTCGGCAAGTGCATTTTCAGGGACATGATGGAATTTGT  
ETCCCTCTTATAGCTTCTGAGAGCTTTCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT  
TTCTTTTCACTGTAGAGCTACTGCAGAACCCAGCCTGAAATCTACTGGATAACACCTTCTG  
GTCAAAAATCTTGCTTAATACCTTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA  
GATATAAATGGCGTAACCTCCAAAGAAGGGGTTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG  
GCTCTTTGAAATATTAATAAGAGATATTGAGGCAATTCAGTTTGGTGTCTTGGAAAGCA  
AGTTTCTAAATCTCAAAATCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAATTTCTCA  
TGCTGCGCAAGTGTCTGAATACCATTCTGATGTCAAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTTGTATTGATATTCACCATCTATCAGAAAAACAGAAAAAA  
TGTGTAAATGTCACCACCAAAGGTTTGCACCCCTGATCAAAAAGAGTATGAAAAGATAATAC  
CACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCTCTTCCAGAAATGAACCTGTGATGGTGGACAGCTATGTGAGGAATTGATTAACAG  
AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCTCTGATAAATCTCTGGGAAGCAGGAAA  
AGAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT  
AAAAACCAAGGAACCAACTCCAAAAATGAAC

## **FIGURE 26**

MKDMPRIHVLLGLAITTLVQAVDKKVDCCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTLPKCLSELNQLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDA  
LPNLLETLMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLEISFYDNRL  
IKVPHVALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGHTIESLPNLKEISIHSPNIRC  
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGNVRQVHFRDMMEICPLIAPESFPPSNLNV  
EAGSYVSFHCRTAEPPQPEIYWITPSGQKLLPNTLTDKIFYVHSEGTLDINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFAV  
KTENSHAAQGARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLGIIGVICLISCLSPENMNCDDGHSYVRNYLQKPTFALGELYPPLIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

### **Signal sequence:**

amino acids 1-22

### **Transmembrane domain:**

amino acids 633-650

### **N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

### **Tyrosine kinase phosphorylation site.**

amino acids 570-579

### **N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

### **Cell attachment sequence.**

amino acids 277-280

## FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTTGA AACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC  
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGATTATGTGACATTCACAGCATGAATCT  
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCCTTA  
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTTGTTCTTCCTCTGGG  
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTTGAGTTTATCGATGAGCAT  
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC  
AACGTGATCTGTAAACGTCCTGTTGGATGAACATGCTGGCAGACCATTCTCTCAATGCTGC  
CAACGACGCTGACCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTTGGCTGGTTCACATATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG  
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCTATTGAGAAAGAAAGAAA  
GTAGTTTGCATGTCAGTAGAAATAAGTGTTTACTTCTCCCATCCATTGTAAACATTTGAA  
ACTTGTATTTAGTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA  
TAAATAATTTAGTTTAGTGATCCACCCCTAATTGTACCCCGATGGTATATTTCTGAGT  
AAGTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAATTTATTTTTT  
AATTTAAAGCAAATAAAGCTTAACTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

## **FIGURE 28**

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSSGGLNVTCSNANLKEIPDL  
PPETVLLYLDNSQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGV AETLQTLDLSDNR  
IQSVHKNAFNNLKARARIANNPW HCDCTLQQVLRSMASNHETAHNVIC KTSVLD EHA GRPFL  
NAANDADLCNLPKKT TDYAMLVTMFGWFTMVISYVVVYVVRQNQEDARRHLEYL KSLPSRQKK  
ADEPDDISTVV

### **Signal sequence:**

amino acids 1-33

### **Transmembrane domain:**

amino acids 205-220

### **N-glycosylation site.**

amino acids 47-51, 94-98

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

### **Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

### **N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG  
GGCGTGAGGAGCATGCCAGCCCTCTTGGCTGCTGGCAGCCATCCTCTGCTGGTGCT  
GGGCTCAGTGCTGTAGGCTCGGCCACGGGCTGCCCGCCCGCTGCGAGTGCTCGCCAGG  
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCAGGGGATCCCCACCGAG  
ACGCGCTGTGAGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTTCGCCAG  
CTTCCCGCACCTGGAGGAGTTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGCG  
CCTTCAACAACCTTCTCAACCTCCGACGCTGGGTCTCCGACGCAACCCTGAAGCTCATC  
CCGCTAGGCGTCTTACTGGCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT  
CGTTATCCTACTGGACTACATGTTTACGGAACCTGTACAACCTCAAGTCACTGGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCTCACCGCGCTTACGCGGCTCAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACGAGGCGCTGTCCCACTGCACGGCT  
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCTTCAAGAGGC  
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC  
TGCCTCTACGGCTCAACCTGACGTCCCTGTCCATCACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCGCTCCGCCACCTAGTCTATCTCCGCTTCTCAACCTCTCTACAACCCCATCA  
GCACATTGAGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGG  
GGGCGAGCTGGCGTGGTGAGCCCTATGCCTTCCGCGGCTCAACTACCTGCGCGTGCTCAA  
TGTCTCTGGCAACAGCTGACCACACTGGAGGAATCAGTCTTCACTCGGTGGGCAACCTGG  
AGACACTCATCTGGACTCCAACCCGCTGGCGTGCGACTGTCCGCTCTGTGGGTGTTCCGG  
TCGCCGTGGCGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCGCGAGTTTGCCA  
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGTACTTGCCCAACTTTCACCTGCCCGCGG  
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACACGCTGCAGTTT  
GTGTCCGGGCGGATGGCGACCCGCGCCGCCATCTCTGGCTCTACCCCGAAGCACTT  
GGTCTCAGGCAAGCAATGGCGGCTCACAGTCTTCCGTAGTGGCAGCTGGAGGTGCGCT  
ACGCCCAGGTACAGGACAACGGCACGTACTGTGCATCGCGGCCAACGCGGGCGGCAACGAC  
TCCATGCCCGCCACCTGTCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAA  
GACCTTTCGCTTTCATCTCCAACAGCCGGGCGAGGGAGAGGCCAACAGCACC CGCGCACTG  
TGCCTTTCCTTCGACATCAAGACCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC  
CTGGCGCTCGTCTCTCTGCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC  
AAAGCACAACTCGAGATCGAGTATGTGCCCGAAAGTCGGACGCGAGGCATCAGCTCCGCG  
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCGGGGGCGGGGGGAGGGACCCCG  
GGCGGCGGGCAGGGGAAGGGGCTGGTGGCCACCTGCTCACTCTCCAGTCTTCCCACTC  
CTCCCTACCTTTTACACAGGTTCTCTTCTCCCTCCCGCTCCGTCCTGCTGCCCCCCG  
CCAGCCCTCACCACCTGCCCTCTTCTTACCAGGACCTCAGAAGCCGAGACCTGGGGACCCCA  
CTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACCAACCGACCGCGCAGAGTCA  
ATAATTCAATAAAAAAGTTACGAACTTTCTCTGTAACCTGGGTTTCAATAATATATGGAATTT  
TATGAAACTTGAATAATAAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 30**

MQVSKRMLAGGVSRMSPSPLLACWQPILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFFNNLFLNRLTL  
GLRSNRKLKLIPLGVFTGLSNLTQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA  
FSGLSLEQLTLEKCNLTISIPTEALSHLGLIVLRHLNINAIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSIHCNLTAVPYLAVRHLVYLRFLNLSYNPISITIEGSMLEHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSGVGNLETILDSNPLA  
CDCRLLWVFRRRNRILNPNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPFPAILWLSPRKHLVSAKSNGLRTVFDPDGTLEVRYAQQVDNGTYL  
CTAANAGGNDSPAHLHVRYSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPPFPDIKTLI  
IATTMGFISFLGVVFLCLVLLFLWSRGKGNTKHNIIEIEYVPRKSDAGISSADAPRKFNMKMI

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 556-578

### **N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
507-611

### **Tyrosine kinase phosphorylation site.**

amino acids 590-598

### **N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## FIGURE 31

CCCACGCGTCCGCACTCGGCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTTCGGTCAAC  
ATCGTAGTCCACCCCTCCCATCCCCAGCCCCGGGGATTCAAGGCTCGCCAGCGCCAGCC  
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCTCGTCTCTGCTCTGCTCTGCTG  
TGTTGCGCTGCTGCTGGGCGCCCGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCTCAAGTGCCAAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTAGCTGGTTACCTCTACGCCCCAGAGGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATCCACAGAAGCCCATCATCACTGGTT  
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCATAACTGTCACTCTTCTGGGAGCAAG  
CCTGCAGCCCGGCTCACCTGGAGAAAGGTTGACCAAGAACTCCACGGAGAACCAACCCGCAT  
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTGAGGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTTCCCTTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG  
CAACATGGGCGAGTACAAGGCCTACTACACCTCAATGTTAATGACCCAGTCCGGTGCCCT  
CTCTCTCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCAATTGTCTTCTGCTG  
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAAGCG  
GCGAGTCAGGAGGGGACGACAAGAAGGAATATTTCATCTAGAGGCGCCTGCCACTTCTCTGC  
GCCCCCAGGGGCCCTGTGGGGACTGTCTGGGGCCGTACCAACCCCGACTTGTACAGAGCAA  
CCGAGGGCCGCCCTCCGCTTGCTCCCCAGCCACCCACCCCTGTACAGAAATGTCTGC  
TTTGGGTGCGGTTTGTACTCGGTTTGAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTTCTCTGCATTGGGTTATTATTATTTTGTAAACAATCC  
CAAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA  
AACAAAAACA

## **FIGURE 32**

MGAPAASLLLLLLFACCWAPGGANLSQDDSQPWTSDETUVAGGTVVVKCQVKDHEDSSLQW  
SNPAQQTLTFGEKRALRDNRILQVLTSTPHELSSISINVALADEGEYTCSTFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLHLCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGYLTHTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 331-352

### **N-glycosylation site.**

amino acids 25-29, 290-294

### **Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

### **N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



## FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTTCTTCTCCTTTCTCTGG  
CTTCGGACATTGGAGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTGTTTGGATTCTGTT  
GCTGGAGACGTCTCTTTGTTTTGCCCCTGGAAACGTTACAGGGGACGTTTGCAAAGAGAAGA  
TCTGTTCTCTGCAATGAGATAGAAGGGACCTACAGTAGACTGTGAAAAAAGGGCTTCACA  
AGTCTCGACGGCTTTCATGTCGCCGACTTTCCGAGTTTTACCATTTATTTCTGCATGGCAATTC  
CCTCACTCGACTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGACATGG  
AAAACAATGGCTTGCATGAATCGTTCCGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG  
CTGCACATCAACAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAACTCATCAGCACCCCTACCTGCCAAC  
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTTGGAGCAAAATCCCTGGTATTGCGGAGATCTGTCTAGAGGATAACCCCT  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAAATGGCTGGA AAAACATTCCCAAGAATGCC  
CTGATCGGCCGAGTGTGCTGCGAAGCCCCACAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACGAGACTTTGTCTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCTG  
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAATGGGCAAGAG  
GATCATGCCACACGAGGCTGTGCTCAAACCGGAGGTACAAGATCCAGGCAACTGGCAGAT  
CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAACCCCTTAGCTAAC  
GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCAGGGTCCGGGTTTAAAGATGAAC  
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA  
GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAACTCGCACTTTGTGGATTACAAGA  
ACCTCATTTCTGTGGATCTGGGCAACAATAACATCGCTACTGTAGAGACAACACTTTTCAAG  
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTAACCTGGACAGCTGTCCCGGGA  
GAAATTGCGGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCCGGGCACTTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAACAACCTG  
CTGAGGTCCTGCCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTTAAACTCAGCCTGCACAA  
CAATTACTTTCATGTACTCCCGGTGGCAGGGGTGCTGGACCAGTTAACTCCATCATCCAGA  
TAGACCTCCACCGAAACCCCTGGGAGTGCTCTGTGCACAATTGTGCCTTTCAAGCAGTGGGA  
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGCTGAACTTCTT  
TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCACGTTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGGAAGCACTC  
AATCCTACCTAGACACCAGCAGGGTGCTCATCTCGGTGTTGGTCCCGGACTGCTGCTGGT  
GTTTGTCACTCCGCTTACCGTGGTGGGCTGCTCGTGTATCTGAGGAACCGAAAGC  
GGTCCAAGAGACGAGATGCCAACTCCTCCGCTCCGAGATTAATTCCTACAGACAGCTGTG  
GACTCTTCTTACTGCGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG  
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGGC  
ATACATCCTTCCCCACCGAGGCCACCCCGGGGCTGGAGGGGCGTGTACCCAAATCCCGCG  
CCATCACTCGGATGGGCATAAGTAGATAAAATACTGTGAGCTCGCAACAACCGAAAGGGCT  
GACCCCTTACTTTAGCTTCCCTGCTTGAACAAGAGCAGACTGTGGAGAGCTGGGAGAGCCGA  
GCCAGCTCGCTCTTGTCTGAGAGCCCTTTTTCAGAGAAAGCCAGCAGACCTGCTGGAAG  
AAGTGACAGTGCCCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCGGGTTCTATAC  
ATATATACATATACCATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGGATTAG  
CCCGGTGATGGCTCCCTGTTGGCTACGAGGATGGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAATAAGTAACCTTGACTTCTGAC

## FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLFPNEFANFYNAVSLHMENGLHEIVPGAFLGLQLVVKRLHINNKKIKSFRKQ  
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLEVLILNDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPLVEEVLBQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNQGEDHATPGSAPNGGK  
IPGNWQIKIRPTAAIATGSSRNKPLANSPLCPGGCSCDHI PGSGLKMMNCNNRVSSSLADLKP  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLLEYLNVEYNAIQILPGTFNAMEPKLRILILNLLRSLPVDVFAGVSL  
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCCTIVPFKQWAERLGSSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL  
VPGLLLVFVTSAPFTVVGMLVFILRNKRKSKRRDANSASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

### Signal sequence:

amino acids 1-15

### Transmembrane domain:

amino acids 618-638

### N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

### Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

### N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

## FIGURE 35

AGTCGACTGCGTCCCTGTACCCGGCGCCAGCTGTGTTCTCTGACCCCAAGTAACACTCAGGGC  
TGCACCGGGCCCTGGCAGCGCTCCGCACACATTTCTGTTCGCGGCTTAAGGGAAACTGTTGGC  
CGCTGGGCCCGGGGGGAATTCTGGCAGTTGGGGGGTCCGTGGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGTTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGGCTCCAGACAC  
AGCTCTGCTCTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGCCCTCAG  
AGAATGAGGGCCGGCGTTTCGCCCTGTGCTCTCTGGCAGGCGCTCTGGCCCGGGCCGGGGCG  
CGGCGAACACCCCACTGCGGACCGTGTCTGGCTGCTCGGCTCGGGGGCTGTACAGCCTGTC  
ACCACGCTACCATGAAGCGGCGAGCGCGCGAGGAGGCGCTGCATCCTGCGAGGTGGGGCGCTC  
AGCACCGTGCCTGCGGGCGCGAGCTGCGCGCTGTGCTCGCGCTCTCTGGCGCAGGCCAGG  
GCCCGGAGGGGGCTCCAAAGACCTGTCTGTTCTGGGTGCGCACTGGAGCGCAGGCGTTCCTCACT  
GCACCCCTGGAGAACGAGCCCTTTGCGGGGTTTCTCTGGCTGTCTCTCGACCCCGCGCGTCTC  
GAAAGCGACACGCTGCACTGGGTGGAGGAGCCCCAACGCTCTCTGCACCGCGCGGAGATGCGC  
GGTACTCCAGGCCACCGTGGGGTTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGTC  
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTTGCGCCGCGCCCGGG  
GCCGCTCTAATTGAGCTATCGCGCGCCCTTCAGCTGCACAGCGCGCTCTGGAACCTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTGCA  
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGCTGCCCTGCC  
GGGAGGTACCTCCGTGCTGGCAATGCGCAGAGCTCCCTAATCGCTAGACGACTTGGGAGG  
CTTTGCGCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGCGCGCTCTGTGTGACCA  
GTGGGGAAGGACAGCCGACCTTTGGGGGACCGGGTGCCACAGGCGCCCGCGGCCACT  
GCAACCAAGCCCGTGCCGAGAGAACATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC  
ACCCTTGTCTCCCTGAACAAGACAAATTCAGTAACATCTATTCTTGAGATTCCTCGATGGGGAT  
CACAGAGCAGCATGTCTACCCCTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCTCTGCGCACTCTCAAGGCTTT  
CGACTCTCTCTGCGGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT  
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTACGAAAGCCCTCTTCCAGCCA  
AGGAAGGAGTCTATGGGCCCGCGGGCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGACAGAG  
CAGAGGTGCTTGTGCGGAGTCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGA  
CATGGGCACTCCTGTGAACAGTTTTCACCTTTTGATGAAACCGGGAAACCAAGAGGAACCTTAC  
TTGTGTAACGACAAATTTGCGAGAAATCCCCCTTCCTCTAAATTCCTTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGAAGTGCCTTTAGGA  
TGGTGATACTGGGGACCGGGTAGTGTCTGGGAGAGATATTTTCTTATGTTTATTTCGGAGAA  
TTTGGAGAAGTGATTGAACCTTTTCAAGACATTTGGAACAAATAGAACACAATATAATTTACA  
TTAAAAATAATTTCTACCAAAATGGAAGGAAATGTTCTATGTGTTTCAAGCTAGGAGTAT  
ATTGGTTCGAAATCCAGGGAAAAAATAAAAAATAAAAAATTAAGGATTGTTGAT

## **FIGURE 36**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAABEACILRGGALS  
TVRAGAE LRAVLALLRAGPGPGGGS KDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPA PRPGA  
ASNL SYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADBIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACATGFE LGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWP I RVDEKLGETPLVPEQDNSVT SIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVIL TMTVLGLVKLCFHESPESSQPR  
KESMGPPGLESDFEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 399-418

### **N-glycosylation site.**

amino acids 189-193, 381-385

### **Glycosaminoglycan attachment site.**

amino acids 289-293

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

### **Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

### **N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## FIGURE 37

CGGACGCGTGGGATT CAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGC CGGCCGCGTATC  
CCCGGCTACCTGGGCGCGCCCGCGGCGGTGCCGCGGTGAGAGGGAGCGCGCGGGCAGCCGA  
GCGCCGCTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGCGGTGTGAGCGCGGTGGGTGCCGA  
GGGCGCTGTGTGCCGCGCGCGCGCCTGGGGTGCAAAACCCGAGCGTCTACGCTGCCATGA  
GGGCGCGCAACGCCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG  
CAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTTCTCGAGTGTACCCTCCAAATAGCAAATGTACTTGGAAAATCA  
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTTCATAGACCTCGAGAGTGCACAC  
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTTGGCCG  
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC  
CCCCAAGTGGCCAGACCGGATTACCTTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC  
CAAGAAATCAGCTTATAGAAATTAAGATTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTTAAATGGCGGGGAAGTCAACGATGCTAGAGAATTTGAAA  
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTCTTATTTCAGT  
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA  
AACTGCCTACAACATACAGAACAGCCTGTCAACACCACATTTCCCTGTAAACACGGGTTTAAA  
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCAACAACCATCACTCGCGATGGGAGTTTG  
CAGGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTACGACAGCGGG  
CAAGAACATGAGTGCCAGGCTGACTGTGCTGTGCAAGCAGTGCCTCTCCTCAGAAGAGGTC  
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCCAAATCATGCCAAACAGC  
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG  
TTAACAGTGAAGTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTCT  
TCTCAGTAGAAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCGAAAGATGG  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT  
TGCTGTGCTCAGAGGAGCAGCTATCTGATTGGAACCTGCCGACTTAGTGCGGTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTATACATCTCTGTAAAAGGAT  
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTTATAGT  
GTTATTTGTTTCACTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGCTCTTGCCTTTCTA  
AATCAATGCTTAATAAAATATTTTTAAAGGAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFVTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVLNFRFIDLES DNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEFNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI  
QFLSDLSTADGFIGHYIFRPKKLP TTTEQPVT TTFPVT TGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLACTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLT VVCKQCPLLR  
GLNYIIMGVGEDGRGKIMPNSFIMPFKTKNQKLLDALKNKQC

### **Signal sequence:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 355-359

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

### **Tyrosine kinase phosphorylation site.**

amino acids 199-208

### **N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

### **Cell attachment sequence.**

amino acids 149-152

## FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGCGCCCCGCGGGCTGGGGCGGTGCTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTACACCTG  
CCGGGACTGGTTGACAGCTTTAAACAAGGGCCTGGAGAGAACCATCCGGGACAACTTGGAG  
GTGGAACACTGCCTGGGAGGAAGAGAATTTGTCCAATAACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCAAGCAGCAGGAGGCCCCGGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGAGGCACCTTCGGGCCCTCCTGC  
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTCGGTGGCTACGGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT  
TTTGGCCCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTTGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCAGAGGGAGCCAACT  
GTGGAGCTGACCAATTTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGTGCATGGGGGCAGGGCCAGGTGCTGTGAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGTGTCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACCACCTGTAGGACCTCCTCCACCCACGCTGCCCCAGAGCTTGGGCTGCCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTGTAGAGTGGGGTAAGCACCCTACCTG  
CCTTACAGAGCAGCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTCTTCACTGGCGGGACTGGCAGGCTTCACAATGTGTGA  
ATTTCAAAGTTTTTCTTAATGGTGGCTGTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT  
TCTGTGTTCAACACATCCCCACACCCCATTGCCACTTATTATTATCTCAGGAAATAAAGA  
AAGGTCTTGAAAGTTAAAAA

## **FIGURE 40**

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEENLSKYKDS ETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCPPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGSGHCD CQAG  
YGGACGQCGLGYFEARNASHLVCSACFGPCARCSGPPEESNCLQCKKGWALHHLKCV DIDE  
CGTEGANC GADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCS PGYQQVGSKCLDVDECE  
TEVCPGENKQCEN TEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDLVVLQQMFPG  
IIICALATLAAKGDLVFTAITFIGAVAAMTGYWLSERSDRVLEGF I KGR

### **Signal sequence:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 372-395

### **N-glycosylation site.**

amino acids 79-83, 205-209

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

### **Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

### **N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

### **EGF-like domain cysteine pattern signature.**

amino acids 181-193



## FIGURE 41

TGAGACCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAGAGGT  
GCCACCCTTGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGETTCAGCCAGAGC  
TTCGAGAGGTGGCCGGCAGGTTCTTGCGTTGGAGGCCAGCACACCTGCTGGTGTTTCGG  
CATGGAGCAGCGCTGCCGCCAACAGCGAGCTGGTG CAGGCCCTGCTGCGGCTCTTCCAGG  
AGCCGCTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCGGGCC  
CGGGTGACCGCTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCTGCCAGAGAGCGGCTGGAAGGCCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTG CAGAGG  
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTTGCCTCGCAGGGGGC  
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACCCCTGGACCTTGGGGACTATGGAG  
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCGCCAGGAG  
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGTGCTGGAGCCCCGGGCTT  
CCTGGCTTATGAGTGTGTGGGCACCTGCGCGCAGCCCCGGAGGCCCTTGGCCTTCAAGTGGC  
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGTGCCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCAACATGAGGGTG CAGAA  
GTGCAGCTGTGCCTCGGATGGTGCGCTCGTGCCAAGGAGGCTCCAGCCATAGGCGCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTCGAGGGTACCAGGAGAGCTG  
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTTGTCTTCTCAGGAATGAGAATCTTTGGCCACTGGA  
GAGCCCTTGCTCAGTTTTCTATTTCTATTATTCACTGCACTATATTCTAAGCACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTGTCATTGTTTACTTGTCTGTGAC  
TGGATCTGGGCTAAAGTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT  
TGTGATCCCAATCCAGATAATAAAGACTTTGTAAAACATGAATAAAACACATTTTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRVSVHESGWKAFDVTAVNF  
WQQLSRPRQPLLLQVSVQREHLGFLASGAHKLVRFASQGAPAGLGEPQLELHTLDLDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPEALAFKWWF  
LGPRQCTIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSASDGALVPRRLQP

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 158-162

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

### **N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

### **Amidation site.**

amino acids 74-78

### **TGF-beta family signature.**

amino acids 282-298

## FIGURE 43

GTCTGTTCCAGGAGTCTCTCGGCGGCTGTTGTGTCACTGGCCTGATCGCGATGCGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT  
GTGAAGTGTCTCTGTGCCTACTCGGCTTTTCTCTCCCGTGTGGAGTGGAAGTTTGACCA  
AGGAGACACCACAGACTCGTTTGCTATAATAACAAGATCAGACTTCTATGAGGACCGGG  
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCTTACAGTTAACATCCCCCTCTCTGCCACCATTGGGAACCGGG  
CAGTGTGACATGCTCAGAACAAGATGGTTCCTCCACCTTCTGAATACACCTGGTTCAAAGAT  
GGGATAGTGATGCCTACGAATCCCAAAGACCCGTGCCTTCAAGCACTCTTCTCTATGTCTCT  
GAATCCCAACAACAGGAGAGCTGGTCTTGATCCCCTGTGAGCCTCTGATACCTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT  
GTGGAGCGGAATGTGGGGTTCATCGTGGCAGCCGTCTTGTAAACCTGATTCTCTGGGAAT  
CTTGGTTTTTGGCATCTGGTTTGCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCCTTACT  
CAGGTGTACCGGACTCTGGCCCTGATGTCTGTAGTTTACAGGATGCCTTATTGTCTTTC  
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC  
ATCTCTCTTCATGCCCTCCCTCCCTTCTTACCCTGCTGAGTGGCCTGGAACCTGTTTTAAA  
GTGTTTATTCCTTCTTTGAGGGATCAGGAAGGAATCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGCAAAAATGGCGGGGTGCGAGGAATCTGCACTCACTGCCACCTGGC  
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTCTCTGTGTAAGTAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG  
TGATGACACTGGGGTCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG  
CCACTGGGATCCCTCTGCTCTGCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT  
GGAAAATGGGAGCTCTTGTGTGGAGAGCATAGTAAATTTTCAAGAACTTGAAGCCAAAAG  
GATTTAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCGTG  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGCGGAGTTGCGGATCAGCCTGACCA  
ACATGGAGAAACCTTACTGGAAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSLAYSGFSSPRVEW  
KFDQGDITTRLVCYNNKITASYEDRVTFLLPTGITFKSVTREDTGTYYTCMVSEEGNSYGEVKV  
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

### **Signal sequence:**

amino acids 1-27

### **Transmembrane domain:**

amino acids 238-255

### **N-glycosylation site.**

amino acids 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

### **Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

### **N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCAATGAGCGCGGTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGCGAGCCCGCTTTCCACCCGACCTCTGCCAGGCCGAGGCCCCAGCTCAG  
GCTCGTGCCACCCACCAAGTTCAGTGCCGACCAAGTGGCTTATGCGTGCCCTCACCTGG  
CGCTGCGACAGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGACGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCCAGCTCCAGCGACGAGCTCGGCTGTGGAAACCAATGAGATCCTCCCGGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCTGGAGAGTGTACCTCTCTCAGGAATGCC  
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCCTCTGTGGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC  
TCAGTGC AAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC  
CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCCTGCTGCTGT CAGAACAGAAGAC  
CTCGCTGCCCTTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACTGCCACAGCCAGAACTGAG  
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL  
RNC SRLACLAGE LRCTLSDDCIPLTWRC DGHPCDPSDELGCCTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 230-246

### **N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

### **Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

### **N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

### **Leucine zipper pattern.**

amino acids 17-39

## FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG  
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGTCATGAGACCCACAGA  
CTCTTGAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGTTTTAGCTGGCGCTGTGCTTCGGCCCTCACAGCTCACGGGCGGGTT  
CGATGACCTTCAAGTGTGTGCTGACCCCGGATTCCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTCTACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAGAGACTGTGTTTTGAAGCATTTAATGGAACCTAGGCTGGATCCCAAGTGA  
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA  
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTCTATGAAGGATTCAAGATCCGG  
TACCCCGACCTACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCC  
GATCTGTCAAGGCTGCCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAACATCTCTGAGC  
TCCAGACCTCCTTCCCGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTAAACTT  
GATGGGTCTGCGTATCTTGTAGTGCTTACAAAACCTTATCTGGTCTGCCAGCCACCCCGGTG  
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGGTACGGAGATTTCTGCT  
GCCACCCGCGGCCTTGTGAGCGCTACAACCAGGAACGTGGTGGAGTTTTACTGCGATCCT  
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTCTTC  
TTATCAAGTCTACTGTCATCAAATCAGAGCAAACGTGCCCCAGCACCCATGAGACCTCCTGA  
CCACGTGGAAGATTGTGGCGTTACGGCAACCAAGTGTGTGCTGGTGTGCTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTC AAGGCCACTTTCCCCCAGGGGGCCTCCCCGGAG  
TTCCAGCAGTGACCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG  
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCCTTAGGCCCGGGTACATGGCCCTCTGTGGGCCAG  
GGGTGCCCTTTACCCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA  
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAA  
GTCTGTATTACCTCCAGGTGCCAAGAGAGCACCCACCTGCTTCGGACAACCTTGACATA  
ATTGCCAGCAGCGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATATGCCACTGGGT  
GTGTTCTTGAAGAACTGAATTGATTAATAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCCTTTCTCTCTGGTTTTAGACAAATGTAACAA  
AGCTCTGATCCTTAAATATGCTATGCTGATAGAGTGGTGGGCTGGAAGCTTGATCAAGTC  
CTGTTTCTTCTTGACACAGACTGATTAATAAATTAAGNAAAAA

## **FIGURE 48**

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDABIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFVGTVISYRCFPFGFKLDGSAYLECLQNLIWSSSFPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFFPSYQVYCIKSEQT  
WPSTHETLLLTWKIVAFTATSLLLVLLLVILARMFQTKFKAHFPPRGPSSSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCLPVDQSPPAYPGSGDITDTPGGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDIISTAAEEVASTSPGIHHAHWVLFRLN

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 325-344

### **N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

### **Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

### **N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405



## FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCGGTGGCCTAGAGA  
TGCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCCGT  
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG  
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC  
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGTTA  
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT  
GCAGGAGGGATGAGAGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA  
AAGTTCAATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT  
CACAAATTAGGAACCTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTGCGTGGTCATG  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA  
CCGGTGCAACATGAAGAACATTTCAATTGCAAATATTTCTGATGAGAAACCAGCAGTTCCTT  
CTAGAGAAGCTGAAGGTGAGGAACAGAGCTGACAAACCTGTACTTCCAGAAGAACACAG  
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT  
CCTAATCCCCCAGCATTCCTTCTCTCTCTTGTGGTCACCACAGTTGTATGTTGGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAAGCAACACACCATC  
TGGCCCTCTCTCACAGGGAAACAGCCCGACCTAGAGGTCTACAATGTCATAAGAAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTTCATTCGAGTGTGTT  
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGAGAGTGGATTGTGACCAATGACATTTATGA  
GTTCTCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAATGAAATATATG  
GTTATTAGGACATATAAAAACTGAAACTGACAAACATGGAAAAGAAATGATAAGCAAAATC  
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT  
GGATGAGCATGTGTTCCCGACGACCTCCTGTTGGACCCCGACGTTTGGCTGTATCCTTTAT  
CCCGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA  
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAAGGGACAGAGCTTTACCTG  
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAACACCACTCTGTTTTCTTGCTCTATACAG  
CAGCACATATATCATACAGACAGAAAAATCCAGAATCTTTTCAAAGCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGGCCAATTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAAGA  
GCAGGAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSI ESEDEQKLEKFIENLLPSDGDWIGLRRREEKQSNSTACQDL  
YAWTDGSGISQFRNWWYDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY  
SDEKPAVPSRBAEGEETELTPVLPEETQEEDAKKTFKESREAAALNLAYILIPSIPLLLLLLV  
VTTVVCWWVICRKRKREQDPSTKKQHTIWSPHQGNSPDLEVYNVIRKQSEADLAETR PDL  
KNISFRVCSGEATPDMDSCDYDNMAVNPSES GFVTLVSVESGFVTNDIYEFSPDQMGRSKES  
GWVENEIYGY

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 117-121, 312-316

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

### **Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

### **N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC  
ATCCGCAAGTTCCCGCGACTTGGGGGCGCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCTCCTCTGCAGCCTCAACCCGAGGGGAGCGAGGGCTTACCACCATGATCACTGGTGT  
GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCTTGACCTCGCTGGCGTACTGCTTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAAACCCCAAGCTATTAGAGGTCACCCCAAACTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTTCTCCTTACGACTCT  
CAATACCATGAGACCACCCTGAAGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT  
GCAGCAAATGTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCTTTTC  
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTG  
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAGGCCATCATCAT  
CCACACTGATGAAGCAGATTGAGAGTCTTGATCCCAACTACCAAGCTGTGGAGCCTGA  
GGCAGAGAACCAGAGGCCGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTGTACCACAAATGGCCACCGTTTGCT  
GTTGACCTGACCATGGAACTTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGACGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT  
TCTTGAATGCCATGTGAGTTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAGCAGGATGTGTTGATT  
TTAAATAAAGTGCCCTTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLMVQVVRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIHTDEADSEVLYPNYQSCWSLRQRTGRRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD  
FFILLDNVAABQAHNLPSCPMKKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPIDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

### **Signal sequence:**

amino acids 1-23

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

### **Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

### **Tyrosine kinase phosphorylation site.**

amino acids 280-288

### **N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

### **Amidation site.**

amino acids 216-220

### **Leucine zipper pattern.**

amino acids 10-32

### **Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT  
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCTAGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTTGCACCAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGGCGCTGGTGGGGGCGCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG  
ATTGTTTCACATGATGAAGATGCTGGGGCATCGTGTGAGAAGCCAGAGAGCTCTTTCTCCCCA  
GTCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAAGTGAA  
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCGCAAGGTGG  
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAAACCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCCTTCA  
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTGCG  
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA  
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTGTTGCTCAGGGGAGGAG  
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCAGACTGCACCCACCAGGAAGA  
TGTGGCTGTCTCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCCTTCAGAGTTGG  
ATCAGAAGTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA  
CCACCTTTCCCTATGTCTCCACATTGCACACAGCAGATTTCCAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACATA  
CACCATTGTCTCTGTTTCTCTGAAGAACTCTGACAAAAATACAGATTTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTTATTACAATAATAAGATAGCAC  
TATGTGTTCAA

## **FIGURE 54**

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELCCGAASGTPSGILYEPFAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEADAGASC  
ENPSSSFSPVPBGVRLADGPGHCKGRVEVKHQNQWYTVCTGWSLRAAKVVCRLGCGRAVL  
TQRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPPDLRLVG  
GDNLCSGRLEVLHKGWVGSVCDNNGEKEDQVVCQLGCGKSLSPSFRDRKCYGPGVGRIWL  
DNVRCSGEEQSLEQCQHRFWGPHDCTHQEDVAVICSV

### **Signal sequence:**

amino acids 1-15

### **Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

### **N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

### **Amidation site.**

amino acids 196-200

### **Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGCACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGCGGCTGCCTGGG  
CGTCTTCGGCTCTTCCGGCTGCTGCAGTGGGTGCGCGGAAGGCCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA  
TGTGGACAAGAGGGTCATGGAGACAACTACTTTGGCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA  
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCACAGCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA  
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTGTGTGAGACTTAAATGGAGATTTGTCTCACAAGTGGG  
AAAGACTGAAGAAACACATCTCGTGAGATCTGCTGGCAGAGGACAATCAAAACGACAACA  
AGCTTCTTCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACT  
AAAACTAGAAATAAACATCTCAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA  
KLVLGCRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAABILQCFGYVDIL  
VNNAGISYRGTIMDITVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGMKSI  
PFRSAYAASKHATQAFDCLRAEMEQYIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAVGGKKKDVILADLLPSLAVYLRITLAPGLFFSLMASRARKERKSKNS

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 104-120, 278-292

### **N-glycosylation site.**

amino acids 228-232

### **Glycosaminoglycan attachment site.**

amino acids 47-51

### **Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

### **Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

### **N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

### **Amidation site.**

amino acids 265-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17



## FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA  
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAATTTCTTCTGGACATCCTC  
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCCTCGTGAAGCTTTTTATTCTTAA  
GAGGAGAAAAATCAGTCACCGCGCAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGAAGGTTGCAAGGTCATACCTTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTTGTCTACA  
CAAGATCCTCAGATTGAAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA  
GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG  
CTGGACATGTCTCGGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGTCTGTGTTGGA  
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG  
TCTGTGTCTCAATTTTCGTAAACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA  
CTCTGGAACCTGAGGAAGTTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG  
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCTGAGCGTTT  
CCTGGCAGTTTTAAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAATAAGCACCTAGTTTTCTGAAAACAGATTACCAGGTTTAGGTTGATGTCATCTA  
ATAGTGCCAGAATTTAATGTTTGAACCTCTGTTTTTCTAATTATCCCCATTTCTTCAATA  
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTTATTAAAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA  
AATTGTACCATAACCGTTTATTTAACATATATTTTATTTTGTATTGCACCTTAAATTTTGT  
ATAATTTGTGTTCTTTTCTGTTCTACATAAAATCAGAAACTTCAAGCTCTCTAATAAAAA  
TGAAGGACTATATCTAGTGGTATTTCACAATGAATATCATGAACTCTCAATGGGTAGGTTTC  
ATCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT  
GCACAGGGAAGCTAGAGGTGGATACAGTGTGCAAGTATAAAAGCATCACTGGGATTTAAG  
GAGAATTTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA  
AA  
AA

## FIGURE 58

MKFLLDIILLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH  
GILTEQKMFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

### **Signal sequence:**

amino acids 1-19

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

### **Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

### **N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

## FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTC  
AGGGAGGAGCACCGACTGCGCCGACCCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG  
TTTCGCTGGTCCTGTGTGATGCGCTGGCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT  
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCAGGAGCTGAACATGA  
AGAGTTATGCCGGCTTCTCACCCGTGAATAAGACTTACAACAGCAACCTTCTCTCTGGTTT  
TTCCACAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG  
AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCCTTATGTTGTGACAAAGTAACATGA  
CCTTGGCTGACACAGACTTCCCTTGACCAACAACGCTCTCCATGCTTTACATTGACAACTCA  
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT  
AGCACGGGATTTATACAGTGCACTAATTACGTTTTTCCAGATATTTCTGAATATAAAAAATA  
ATGACTTTTTATGTCACTGGGAGTCTTATGCAGGGAATATGTGCCAGCCATTGCACACCTC  
ATCCATTCCCTCAACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA  
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT  
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC  
AGGAAGCAGAAGTGGTTTGGAGCCCTTGAATACTGGATAAACTACTAGATGGCGACTTAAC  
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAAATTTTTCGGGT  
GCCACGGAACCTGAGGATCAGCTTACTATGTGAAATTTTGTCACTCCAGAGGTGAGACAA  
GCCATCCACGTGGGGAATCAGACTTTAATGATGGAACATAGTTGAAAAGTACTTGCAGAGA  
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA  
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC  
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAAGATCTTTAA  
ATCTGACAGTGAAGTGGCTGTTACATCCGGCAAGCGGGTGACTCCATCAGGTAATTATTTC  
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA  
TTCATTTATGGAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCAAAAGAGAACAT  
CAGAGGTTTTTCATTGCTGAAAGAAAAATCGTAAAAACAGAAAATGTCTAGGAATAAAAAAA  
TTATCTTTTCATATCTGCAAGATTTTTTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGC  
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA  
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAAATGA  
AATTTTAGGCTCTGAAATAGGAAGTTTAAATTTCTTCTAAGAGTAAGTGAAAGTGCAAGTTG  
TAACAAACAAAGCTGTAACTCTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT  
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAATAAATGGATGAAGCTATAA  
TAGTTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA  
AAAAATATTATATATAAAGTAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGPGCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRSL  
VGFPFGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTNSMTLRDRDFPWTTLTSLMLYIDNPVGTGFSFTDDTHGYAVNEDDVARLDLYSALI  
QFQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLPVREVKNLNGIAIGDGYSDPESIIG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNV  
TGCSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLRDVTQSVK  
PWLTEIMNNYKVLIIYNGQLDIIVAAALTERSLMGMDWKGSGQYKKAEEKVVKIFKSDSE  
VAGYIRQAGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

### **Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

### **Tyrosine kinase phosphorylation site.**

amino acids 423-432

### **N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

### **Serine carboxypeptidases, serine active site.**

amino acids 200-208

### **Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGACATGTGGGAATCCCACTCTTGTGGCTACAACAT  
TTTTCCCTTTCTCAACAAGTTCTTAACAGTTCTTCAACAGCTAGTAGTACAGGGGTCTCTCT  
GCTGGAGAAGAAAGGGCTGAGGCGAGAGCAGGCGACTCTCACTCAGGGTGACAGCTCTCTTG  
CTCTCTGTGGATAACACAGACATGAGAAATGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAATAGGAAGGAATTTTGTGTCAATATCAGACCTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGGAGGGCTGCCATAACAAGCTTTTAAAAAAGCAGGAGCGACTTCCACTGGGCTGGAT  
AAGACGTGCGCGGTAGGATAGAGGAAGACTGGGTTTAGTCTTAAATATCAATAGCTGGCTGG  
TGAACCTCAACAGCCTTTTAACCTCTCTGGAGATGAAACAGTAGGCTTAAAGGGCCGAGAA  
TAGAGATGCTTTGTAATAATAAATTTTAAAAAAGCAAGTATTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAAGGATTCCCTGAACATCTTCAAGAGGGGAGAAATGTTTAAATAA  
GAAAACCAAAATGTCAGAAAGGAGAGACTCACAGAGCTAAACAGGATGGGCACTGGGTC  
AGGCCAGCTCTTTGCTCTCTCCCGAAATATTTTGGTCTGACCACTCTGCCTTGTGTTTT  
GCAGATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACAACAGAGCCGCT  
CCTCACCGCGGCCCTCTCAGCATGGAACAGAGGCGACCTTGGCCCCGGGCGCTGGAGGTGG  
ACAGCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGGCTGGCCCCCCAGCAGCGCG  
ATGCTCAGGTTCAGCACTTCCACTCTGAGATCTGTAGTGCATCTCAACCACTTGACCGT  
CCACCAGGGACGGGGGGCGCTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCTATAAGACAGGGCCAGGAAGGACAACAAGTCTCGTTAACCCG  
CCCCCTCATGTGCGAGCCTCGACGGAAGTGCTACCCCTCAACAAATGTCAACAAAGTCTG  
CATCATCTGACTACTGTAGAAGACGCCCTGCTGGCTGTGGGAGCTCTTACACAGGGGGTCTGCA  
AGCTGCTGCGCTGGATGACCTCTTCACTCTGGTGGAGCCATCCCAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGTGATTTGTCCTCTGAGGGTGAGGA  
TGGAAGCTCTTCTATCGGCACGGCTGTGGATGGGGAAGCAGGATTACTTCCGAGCTGTCTCA  
GCGGGAAGCTGCCCCGAGAGCCTTGAGTCTCAGCAGTGTCTGACTATGAGCTACACAGCAT  
TTTGTCTCTCTCTCATCAAGATCCCTTCAGACACCCCTGGCCCTGGTCTCCCACTTTGACAT  
CTTCTACCTCTACGGCTTTTGCTAGTGGGGCTTTGTCTACTTTCTACTGTCCAGCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCACTACTCAGCATCTGTGGCG  
CTCTGCAAGATGACCCCTCAAGTTTCACTCATAGCTGTCCCTGCGCTTGGGTGACACCGGG  
CGGGGTGGGAATACGCTCTCGACGGTCTTACTTGGCCAGCTGGGGACTCAGTGGCC  
AGGCTCTCAATATCACCAGCCAGGACAGTGTACTCTTGGCCATCTTCTCCAAAGGCGAGAG  
CAGTATCACCACCCCGCATGACTCTGCCCTGTGTGCTCTCCCTATCCGGCCATCAACT  
GCAGATCAAGGAGCGCTGCAGTCTGCTACAGGGCGAGGGAACCTGGAGCTCACTGGC  
TGCTGGGGAAGGAGCTGTCAAGTGACGAGGGCGCTGTCCCATGCGATGATATCTTCTGTGGA  
CTGACATCAACCAAGCCCTGGGAGCTCAACTCAGTGGAGGCTGACCTTCACTACAC  
CAGCAGGGACCGCATGACCTCTGTGGCTCCTACGTTTACAGCGCTACAGCGTGGTTTTT  
TGGGGAATAAGGTGGCAAGTGAAAAGGTGAAGTCTATGAGTTCAGATGCTCCATGCC  
ATTCACTCTCTCAGCAAAAGTCCCTTTGGAAGTAGTACTTTGGTGAGATTTAACTATG  
GCAACTTTATTTTCTTGGGGAACAAAGGTGCAAAATGGGGAGGTAAGAAGGGGTAAATTTTGT  
ACTAGCTCTTCTAGCTACTCTCCAGCCTCAGTCATGGGTATGGAAGATGCAAGCGCTA  
TTTCAATATTTCCCAACTTTAAGAAAAAATTTAAGAAGGTACATCTGCAAAAGCAAA

## **FIGURE 62**

MGTLGQASLFAPPNGYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENDRWTFNHLTVHQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEDNKSRYPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLAGCSL  
YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLRDPRESSAMLDYELHSDVFSSLIKIPSDTLALVSHFDIFYIYGFSGGFVYFL  
TVQPETPEGVAINSAAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAAQAFNITSQDDVLFAIFSKGQKYHHPDDSAFCAPPIRAINLQIKERLQSCYQGEEN  
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLTYTTSRDRMTSVASYVYNG  
YSVVFVGTKSGKLKKVRVYEFRCNSNAIHLLSKESLLEGSYWRWFNYRQLYFLGEQR

### **Signal sequence:**

amino acids 1-32

### **Transmembrane domain:**

amino acids 71-87

### **N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

### **Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

### **N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## FIGURE 63

AGGCTCCGCGCGCGGCTGAGTGCAGTCTGGAGTGGGAACCGGGTCCCCGCGCTTAGAGAACACGCGATGACCA  
 CTGGAGACCTTCGCGCGAGGCGCGGCCGACGCTGGGACTCTGCTGCTGGTCTGCTCTGGGCTTCTCTGGTCTCC  
 GCAGGCTGGACTTCGGAGCACCTTGGTCCCTCTGCGGCTCGCCATCGACAGCTGGGGCTGGGCAAGGCGTGGAA  
 ACTTCATGCTCGAGGATTCACCTTCTGGATCTTCGCGGCTCCATCCACTATTTCGCTGGCCGAGGAGTACT  
 GGAGGGACCGCTGCTGAAGATGAAGGCTTGGCTTGAACACCTCACCACTTATTCGCTGGAACTTGCATG  
 AGCCAGAAAGAGGCAAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCTTCTGCTGATGGCCGACAGATCG  
 GCGTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGCTTGCCTCAGCTGGCTAC  
 TCCAGACCTTGGCATGAGCTGAGGACAACTTACAAGGCTTCAACGAAGCAGTGGACCTTATTTTGGACCACT  
 TGATGCTCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGACCTTATCTTGGCGTGCAGTGAGGAATGAATATG  
 GTTCCCTAATAAAGACCCCGCATACATAGCCCTACGCTCAAGAAAGCACTGGAGGACCGTGGCATTTGTGGAATCTGC  
 TCTTGACTTTCAGACAACAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTGGCCACCTTGCATTCAGT  
 CAACACACGAGCTGCACTACTGACCACTTCTCTTCAACGCTCCAGGGGACTCAGCCCAAGATGGTGTGGAGT  
 ACTGACCGGGTGGTTTGAATCTGCTGGGGAGGCCCTCACAATATCTTGGATTCTCTGAGGTTTGAACACCGTGT  
 CTGCCATTTGTGGACGCGCGCTCTCCATCAACCTCTACATGTTCCACGGAGGCCAACCTTTGGCTTCATGAATG  
 GAGCCATGCACTTCCATGACTACAAGTCAGATGTACCAGTATGACTATGATGCTGTGCTGACAGAAAGCCGCG  
 ATTACACGCGCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCACTCCCTCTCCCTCCCCACCTG  
 ACCTTCTTCCCAAGATGCGGTATGAGCCCTTAAACGCCAGTCTTGATCCTGTCTGTGGGACCGCCTCAAGTACC  
 TGGGGAGGCCAATCAAGTCTGAAAGCCCTCAACATGGAGAACCTGCGAGTCAATGGGGGAAATGGACAGTCTCT  
 TCGGGTACATTCTCTATGAGACCGCATCACCTCGTCTGGCATCCTCACTGGCCAGCTGCGATGATCGGGGGCAGG  
 TGTTTGTGAACACAGTATCCATAGGATTTCTGGACTACAAGACAACGAAGTCTGCTCCCTTCCTCAGGGTT  
 ACACCGTGCTGAGGATCTTGGTGGAGAAATCGTGGCGAGTCAACTATGGGAGAAATATTGATGACCAAGCGCAAG  
 GCTTAAATGGAAATCTCTCTCTGAATGATTACCCCTGAAAACTTCAGAATCTATAGCCTGGATATGAAGAGA  
 GCTTCTCAGAGTTCTGGCTTGAACAAATGGNGTTCCCTCCGAGAAACCCACATACCTGCTTCTCTTTGG  
 STAGCTTGTCTACAGCTCCAGCCTTGTGAZCACTTTCTGAGCTGGAGGCTGGGGAAGGGGTTGTATTCA  
 TCAATGGCCAGAACTTGGACGTTACTGGAACATTGGACCCGAGAAAGCGCTTACCTCCAGGTCCTCGTTGA  
 GCACGGGAATCAACAGGTATCTGTTTTTGGAGAGCATGGCGGCCCTGCATTACAGTTACGGAACCCCC  
 AACCTGGSCAGGAACCGATACATTAAAGTGAACGGTGGCACCCCTCTCTGCTGGTCCAGTGGGAGACTGCGCCCTC  
 CTCTTGACCTGAAACCGCTGGTCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAAGTAGCAACCTCAGGG  
 ACTGGGGGCTCAGTCTGCCCCTGTCTCAGCTCAAAACCTTAAGCTCGAGGAAAGGTGGGATGGCTCTGGGCC  
 TGGCTTTGTGATGATGGCTTCTACAGCCCTGTCTTGTGCCAGGCTGTGCGGCTGTCTCTAGAGGTGGGAGC  
 AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAGAGTGTGAAACGTGCCCTTGCACCGGACGTCACAGCCC  
 TGGCAGACTCTGCTGGACTCAGGCGTGCTTTGTCTGGTTCTGGGAGGCTTGGCCATCCCTCATGGCCCCAT  
 TTTATCCCCGAAATCTGGGTGTGTCAACAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT  
 CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA  
 CATCCAGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCAACATCC  
 AGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCAACATGGGAGG  
 GAGGAGCAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCAACATGGGAGGAGG  
 ACAGAAGGCCAGCTCAGTGGCCCCGCTCCCCACCCCGAACCGCCGACAGCAGCAGCCCTCTCTC  
 GAAGTGTCTCAAGTCCGATTGTAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCAGTGTCTGTA  
 GTTGAGTAAAGCTATAACCTTGAATCAAA

## **FIGURE 64**

MTTWSLRRRPPARTLGLLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW  
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDPSGNLDLEAFVLMA  
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGTFEAVDLYFDHLSRVVPLQ  
YKRGGPPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKDGLSKGIVQGVLAT  
INLQSTHELQLLTTFLFNVQGTQPKMVMMEYWTGWFDWGGPHNILDSSSEVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFDYKSDVTSYDYDAVLTEAGDYTAHYMKLRDFFGSGISGIP  
LPPPPDLPLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFQYILYE  
TSTTSSGILSGHVHDRGQVFVNTVSI GFLDYKTKIAVPLIQGYTVLRLIVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSP LKNFRIYSLDMKKSFFQRFGLDKWXSLEPETPLPAFFLGSL SIS  
STPCDTFLKLEGWEKG VVFINGQNLGRYWNIGPQKTLYLPGPWLSGGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

**N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,

320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586



## FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC  
CTGTTGAGGGTCTCTACTTTGGCCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCAGGACCCTCCATCTCCCAATGTTGGAGGAATC  
CGACCACTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTTAACACGCCATTGGCTCCC  
AAGAAGCTGTCTGCTTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA  
GGCAGACACTCGGTTCGTTTCGTAGTGGATAGGGGTCAAGCCGTTTCTCTAGACGGGGCC  
CGTTCGCTATGTGTCTGGCAGCTGCCTACTTTCGGGTACCGCGGTGCTTTGGGCCGAC  
CGGCTTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTATGTGCCCTGGAACTA  
CCACGAGCCACAGCTCGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCCTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTCACTAGAGACCAGGACCTTACATCTGTGCAGAG  
TGGGAGATGGGGGTCTCCCATCTCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC  
AGATCCAGACTTCTTGGCGCAGTGGACTCTGGTTCAAGGTCTTGTGTCGCCAAGATATATC  
CATGGCTTTATCACAATGGGGCAACATCATTAGCATTCAGGTGGAGAAATGAATATGGTAGC  
TACAGAGCCTGTGACTTTCAGCTACATGAGGCACCTGGCTGGGCTCTTCGCTGCACTGCTAGG  
AGAAAAGATCTTGGCTCTTACCACAGATGGGCCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GACTCTATACCACCTGTAGATTTTGGCCCAGCTGACAACATGACCAAAATCTTTACCTTGCTT  
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAACCAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTAACATGTACATGTTCCATGGAGGTACCAACTTGGGATATTGG  
AATGGTGCCGATAAGAAGGGACGCTTCTTCCGATTACTACCAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTGTCTCTCGAGATGTCTATCAGCAAGT  
TCCAGGAAGTTCTCTTTGGGACCTTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG  
ACTCTGCACCTGGTTGGGCATTACTGGCTTCTCCTAGACTTGCCTTGGCCCCGTGGGCCATC  
TCATTCATCTTGGCAATGGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTTCATGTGTACC  
GAACTTATATGACCCATACCATTTTGGAGCCAACACCATTCCTGGGTGCCAAATAATGGAGTC  
CATGACCGTGCTATGTGTATGGTGGATGGGGTGTTCAGGGTGTGTGTGGAGCGAAATATGAG  
AGACAAACTATTTTGGAGGGGAACTGGGGTCCAAACTGGATATCTTGGTGAGAACATGG  
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGAATTCAGGGGCTGTGTAAGCCACCAATTCTG  
GGGCAACAATCTTACCAGTGGATGATGTTCCCTCTGAAAATGATAACCTTGTGAAGTG  
GTGGTTTCCCTCCAGTTTGGCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT  
ACTCCAAACATTTTCCAAATTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG  
ACCAAGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCCGGTACTGGACAAAGCAGGGGCC  
ACAACAGACCCTCTACGTGCCAAGATTCTCTGTGTTTCTAGGGGAGCCCTCAACAAATTA  
CATTGCTGGAAGTCTAGAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGGATAAGCCTATC  
CTCAATGACTAGTACTTTTGCACAGGACACATATCAATTCCTTTTCAGCTGTATACACTGAG  
TGCCCTCTGAACCAATGGAGTTAAGTGGGCACCTGAAGGTAGGCCGGGATGGTGGCTCATGC  
CTGTAATCCAGCACTTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTGAGGACTCAAGA  
CCAGCCTGGCCCAACATGGTGAAACCCCGTCTCCACTAAAAATAAAAAATTAGCCGGGCGTG  
ATGTTGGGCACCTCTAATCCAGCTACTTGGGAGGCTGAGGGCAGGAGAAATGCTTGAATCC  
AGGAGCAGAGGTTGCAGTGGAGGTTGTACCATGCATCTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAA

## FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKGASVNMYMFHGGTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVFN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWYPQAPSGPTFYSKTFPILGSGVGDFTFLYL  
PGWTKGQVWINGFNLGRYWTQKGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC  
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT  
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT  
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTTGGTGTGTT  
CTGTGCAGAAGTTAGTGAAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG  
AAAACTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTTCATG  
CTGTCGGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAAATTCTGTCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCATCACTTGAGA  
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTTGCTCAAAAA  
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACCTCTGAAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTTCCACGTGAAGAGCAATTTGACCAAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC  
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGCTGCTGAGCTGGAATCCAGA  
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAAGTGGAT  
TTAAAGTCCAATAACATTTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT  
GACTTGTTTAAAATATATGGCATAACAAAATTGTTACTATTCTCTCCTCTATTACCCATGTCA  
AAAAGTGGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT  
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTGTCATATCACTGGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAAGTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG  
CTTGAGACCGCTGCCAGCCCAGCTGGGCCAGTGTCCGGATGTCAAGAAAAGCGGGCTTGTG  
TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCCTTTGCAATGGGATTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC  
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG  
ATACATCTTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCATGTTTGTAGGGTTTTAAGTCATTCAATTCCAAATCATTTTTTTTTTTCTTTTGGGG  
AAAGGGAAGGAAAAATTATAACTACTAATCTTGGTCTTTTTTAAATTGTTTGAACCTTGGAT  
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAGATAATGATTAAATTGACATT  
TTCTTACTAAAAA

## FIGURE 68

MAYMLKKLLISYISIIICVYGFICLYTLFWLFRIPLKKEYSFEKVRRESSFSIDIPDVKNDF AFL  
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTFEKL RQHISR NAQDKQELHLFMLS G  
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLELRLHLKILHVKSNTLTKVPSN  
ITDVAPHLTCLVIHNDGTCLLVLSLKKMMNVAELELQNCBLERIPHAIFSLSNLQELDLKS  
NNIRTIBEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLES LPVAVFSLQ  
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLSOLTQLELKGNCCLDR LPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP  
FANGI

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

### **Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

### **Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

### **N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## FIGURE 69

CCCACGGCTCCGGCCTTCTCTCTGGACCTTGCATTTCACATTCCTTTTCATTGACAAACTGACTTTTTTTATTCTT  
 TTTTTTCCATCTCTGGGCGAGCTTGGGATCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATTAAGGAT  
 CTGTGTTTGGGGTTTCTTCTCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTGGGGAGGAGACCACGTGG  
 GCTCAGTCTTGGCTTGCACTTATCTGCCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCTCTGC  
 ATCCCTGGTGGTATCCTTGGCGGCTTGTCTCTGCTGATAGTTGCTGTCTGTCTTTACTTCAAAATACACAAC  
 GCGCTAAAAGCTGCAAGGAACTGGAAGCTGTGGCTGTAAAAAATCACAAACCCAGACAAGGTGTGGTGGGCCAAG  
 AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTGTCTGCCCTGCAGTGTCTGGAAGGATATAGAATGTGTGCC  
 AGTTTGTATCTCCCTGCCACCTTGTCTGTGCGACATAAATGAGGGCTCTGAGTTAGGAAGGCTCCCTTCTCAA  
 GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAAGGCACAGAAAGAAAGCAG  
 CTCGCCCATCAGTTTCAATGGAATAAATCAGTGCCCTGCTGGGAACAGCTGCTGGAGATCCCTACAGAGAGCTTC  
 CACTGGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCTCACTGTGGGAATGCTGATAAACAGTCA  
 CACAGCTGCTTATTCTCACACAAATCTACCCCTTGGTGGCTGGAACCTGACGTTTCCCTGGAGGTGTCAGAAA  
 GCTGATGTAAACAGAGCCTATAAAAGCTGTCGCTCCTTAAGGCTGCCAGCGCTTGCCTGCAAAATGAGCTTGT  
 AGAAGGCTCATGCCATTGACCCCTCTTAATTCTCTCCTGTTTGGCGGAGCTGACAAATGGCGAGGCTGAAGGCAAT  
 GCAAGCTGCACAGTCAGTCTAGGGGGTCCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC  
 AGTGAGAATGCACTTGCAAAATAGAAAGACAGAAAACAAAGCATCAGAATTATCTTTTCTTATGTCCAGCTT  
 GATCCAGATGGAAGCTGTGAAAGTGAAAACTTAAAGTCTTTGACGGAACCTCCAGCAATGGGCTCTGCTAGGG  
 CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTGAAATCATCATCCAGTACATTGACCTTCAAAATAGTTACT  
 GACTCAGCAAGAAATCAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCTTAACATCTCTATTCCAAACTGT  
 GGGCGTTACTCGGATACCTTGGGAAGGATCCTTACCAGGCCCAATTAACCAAAGCCGACTCTGAGCTGGCTTAT  
 TGTGTGTGGCACAATCAAGTGGAGAAAGATTACAAGATAAACTAAACTTCAAGAGATTTCTGTAGAAATAGAC  
 AAACAGTGCAGAAATTTGATTTTCTTGCCATCTATGATGGCCCCCTCCACCAACTCTGCGCTGATTGGACAAGTCTGT  
 GGCCGTGTGACTCCCACTTCCGAATCGTCATCAAACTCTCTGACTGTCTGTGTGCTGATCAGATATTGCCAATTCT  
 TACCCGGGATTTTCTGCTTCTTACACCTCAATTTATGCGAGAAACATCAACACTACATCTTTAACTGTGCTCTTCT  
 GACAGGATGAGAGTTATTATAAGCAAACTCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCACATCAAA  
 GACCCCACTTGCAGACCAAAATATCAAAATGTTGTGGAAATTTCTGTCCCTTTAATGGATGTGTGACAAATCAGA  
 AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTCTGTCATCTCTCAACTCTGGAAGTGATCACC  
 CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAAATCTACAGTGGAGATAATATACATAACA  
 GAAGATGATGTAATACAAAGTCAAAATGCACTGGGCAAAATATAACACCAAGCATGGCTCTTTTGAATCCAAATTC  
 TTTTCAAAAGACTATACTTGAATCACCATATTATGTGGATTGGAACCAAACTCTTTTGTTCAGGTAGTCTGCAC  
 AACTCAGATCCAAATTTGGTGGTGTCTTGATACCTGTAGAGCCTCTCCCACTCTGACTTTGCATCTCCAAACC  
 TACCACTTAATCAAGAGTGGATGTAGTCGAGATGAACTTGAAGGTGTATCCCTTATTGTGACATATGGGAGA  
 TTTCCAGTTTAAATGCTTTAAATTTCTTGAGAAATGATGAGCTCTGTGTATCTGCAGTGTAAAGTTTGTATGTGAT  
 AGCAGTGACCACAGTCTCGTGCAATCAAGGTTGTGTCTCCAGAAGCAAAACGAGACATTTCTTATATAAATGG  
 AAAACAGATTCATCATAGGACCACTTCTGTCTGAAAAGGGATCGAAGTGCAGATGGCAATTGAGGATTTGAGCAT  
 GAAACACATGCGGAAAGAACTCCAAACGACCTTTCAACAGTGTGCATCTGTTTCTCTCATGTTCTAGCTCTG  
 AATGTGTTGACTGTAGCGCAATCACAGTGAGGCATTTTGTAAATCAACGGGACAGACTACAAATACCAAGAGCTG  
 CAGAACTATTAACCAAGGTTCAACCTTAAGTGAGACATGTTTCTCAGGATGCCAAAGGAAATGCTACTCTGT  
 GGCTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACAGAGCCTGCATGTAAAAAA

## **FIGURE 70**

MELVRRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIFSYVQLDPDGSCSENIKVFDGTSSNGPLLQVCSKNDYVPVFESSSSTLT  
FQIVTDSARIQRTVFVFYFFSPNISIIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIFYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVVISKSYLEAFNSNGNNLQLKDPTRCP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITROKQLQIIIVKCEMGHNST  
VEIIYITEDDDVIQSQNALGKYNTSMALFESNSFEKTILESPIYVDLNLQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFASTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL  
QCKVLICDSSDHQSRNCNGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVAITTVRHFVNQRADYKYQLQNY

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domain:**

amino acids 571-586

### **N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

### **Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

### **N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
GGACATGCGGCCCCAGGAGCTCCCGAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGCTG  
TGCTGCCGCGCGCCGCTGCCCTGCCACAGCGCCACGCGCTTCGACCCCACTGGGAGTCC  
CTGGACGCGCCGCGCAGCTGCCCGCGTGGTTTGAACAGGCCAAGTTCGGCATCTTCATCCAATG  
GGGAGTGTGTTCCGTGCCCAGCTTCGGTAGCGAGTGGTTCGGTGGTATTGGCAAAAGGAAA  
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT  
TTTGGACCACTATTACAGCAAAATTTTTTAATGCCAACAGTGGGCAGATATTTTTCAGGC  
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT  
CAGAATATTCTGTGGAAGTGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAAGTACCTGCGCTTTGGACTGTACTATCCCTTTTGA  
ATGGTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG  
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCCTGGTT  
ATATAATGAAAGCCAGTTCCGGGCCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA  
TCTGTAAGCATGTTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA  
CATAAATGGAAAACTGCATGACAAATAGACAACTGTCTGGGGCTATAGGAGGGAAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAAATGGTGAAGCAACTGTAGAGACAGTTTCATGTG  
GAGGAAATCTTTTGATGAATATGGGCCACACATAGATGGCACCATTCTGTAGTTTTTGAG  
GAGCGACTGAGGCAAGTGGGGTCTGGCTTAAAGTCAATGGAGAAGCTATTTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCAACCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTTTCTTAAATGGCCCACTCAGGACAGCTGTTCCTTGGCCAT  
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG  
GATTTCTTTGGAGCAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC  
CGTGAAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACTGGATAAGAAAATTTATTTGGCAGTTGACGCCCTTCCCTTTTCCCACTA  
AATTTTCTTAAATTACCCATGTAAACATTTTAACTCTCCAGTGCACTTTGCCATTAAAGTC  
TCTTCACATTGATTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTACATTATAGTAG  
CAAGGAATTTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGCTAGTCAAT  
TTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAACATAGAGAAG  
GTACAGTAAAAATCTGTAATAATAATGGTGCACTGTATAGGGCACTTACACAGAAATGGAG  
CTTACAGGCTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAACTACTGTATGCTTAGGCTACACTACATTTATAAAAAAA  
GTTTTTCTTCTTCAATTATAAATTAACATAAGGTACTGTAACCTTACAAACGTTTTAATT  
TTTAAACCTTTTGGTCTTTTGTAAATACACTAGCTTAAACATAAACTCATTTGTGCA  
ATGTA

## FIGURE 72

MRPQELPRLAFPLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSFGSEWFWWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRDRLRFGLYYSLFEW  
PHPLFLEDESSSPHKRQFPVSKTLPELYELVNNYQPEVLWSDGDDGAPDQYWNSTGFLAWLY  
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMITDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGNNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT  
WRSQNDTVPDVMYTSKPEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKGWALALTNI

### **Signal sequence:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

### **Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

### **Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

### **N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

### **Leucine zipper pattern.**

amino acids 410-432

### **Alpha-L-fucosidase putative active site.**

amino acids 283-295



## FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC  
TGAGGTGTTTCCTTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT  
TTCCATCCAGGTGTCAATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCCAGC  
AGCTGAATTTACAGAAGCTTAAGGAGGCTGTAGGCTGTCTGGGACTAAGTTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGA  
TGGATTCTGGTCTATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG  
TCCTGAATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTTCAACTCATCTGAT  
ACTTGGACTAACTCGTGCATTCCAGAAATATCACCCAAAGATCCCATATTCAACACTCA  
AACTGCAACACAAACACAGAATTTATTGTGAGTGCAGTACCTACTCGGTGGCATCCCCCT  
ACTCTACAATACCTGCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGG  
AGAAAAAATTGATTTGTGTACAGAAGTTTTTATGAAAACTAGCACCATGTCTACAGAAAC  
TGAACCAATTGTTGAAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTC  
CCACGGCTCTGCTAGTGCTTGTCTCTCTCTTCTTGTGTGTCAGCTGGTCTTGGATTTTGC  
TATGTCAAAAGGTATGTGAAGGCCCTCCCTTTTACAAAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCATAAGAGGAATCAAAAGA  
AAACTGATAAAAAACCAGAAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCAGTGCCGTGGA  
GCTGAAGTTT<sup>1</sup>TAGATGAGACAGAATGAGGAGACACACTGAGGCTGCTTCTTCTCATGCTCC  
<sup>2</sup>TTACCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAGAAGTCCACCTT  
<sup>3</sup>GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAATGC  
<sup>4</sup>CCTTCTCCTTATTGTAAACCTGTCTGGATCCTATCCTCCTACCTCCAAGCTTCCACGGCC  
<sup>5</sup>TTTCTAGCCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTGTCAAAGTGCAA  
<sup>6</sup>GGACCTAAAACTCTCATCAGTATCCAGTGGTAAAAAGGCCCTCTGGCTGTCTGAGGCTAGG  
<sup>7</sup>TGGGTTGAAGCCAAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGAGCTCAGAC  
<sup>8</sup>CCTTCTCTCAGCTCTGAAAGAGAAACACGTATCCCACTGCATGTCTTCTGAGCCCGGTA  
<sup>9</sup>AGAGCAAAAGAATGGCAGAAAAGTTAGCCCCGAAAGCCATGGAGATTCTCATAACTTGAG  
<sup>10</sup>ACCTAATCTCTGTAAAGCTAAAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTACCT  
<sup>11</sup>GTGACAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGAAACACATTGAGTTGGA  
<sup>12</sup>ATCACTGTTTGAACACACACACTTACTTTTTCTGGTCTCTACCCTGTGATATTTTCTCT  
<sup>13</sup>AGGAAATATACTTTTACAAGTAACAAAAATAAAACTCTTATAAATTTCTATTTTATCTGA  
<sup>14</sup>GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTAAAAAGTAATAAAATTCA  
<sup>15</sup>ACAAACATTGTCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTCTGTAAT  
<sup>16</sup>TGAATATTATTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAGCTATTTTTTCA  
<sup>17</sup>GTTTTGATATTTCTAGCTTATCTACTTCCAACTAATTTTTATTTTTGTCTGAGACTAATCTT  
<sup>18</sup>ATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTACATACCTAAGAAG  
<sup>19</sup>TACATTTGTACCTCTATATACCAAGCACATTTTAAAAAGTGCCATTAAACAAATGTATCATA  
<sup>20</sup>GCCCTCCTTTTTTCCAAAGAAGGACTGAGAGATGCAGAAATATTTGTGCAAAAAATTA  
AGCATTAGAAAACCT

## **FIGURE 74**

MARCFSLVLLLSIWTTTRLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQF  
AAVCYNSSDTWTNSCIPBIIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFPFNTNKNQKEMIETKVVKEEKANDSNPNEESKKTDKNPESKSP  
SKTTVRCLEAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 75

AGATGCGCGTCTTGGCACCTCTAATTGCTCTCGTGTATTTCGGTGCCGCGACTTTTCACGATGG  
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCTTCTTACTCGTGAGGAA  
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAAACAAT  
TCTTTTCTTCCGCTTGGATATTGCGATGGGCCTACTTTACATCACACTCTGCATAGTGTTC  
TGATGACGTGCAAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAAGTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA  
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC  
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC  
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCTGATCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG  
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACGACGGGCCAAGAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA  
TGGGGAAAACAAGAAGGATAAA**TAA**GATCCTCACTTTGGCAGTGCTTCCTCTCTGTCAATT  
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNNATNNATGTTTTCCCTTTGG  
CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG  
GCACCTACAGGAAGGCCTGCCATGCTGTGGCCAACTGTTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGAGGGGGAAATGTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATC  
AGCTATTGAGACATCTCCATGTTTCTCCATGAACTCTGTGGTTTCATCATTCCTTCTTAG  
TTGACCTGCACAGCTTGTTTAGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAA  
CGCTAAGAAATTTCCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC  
TTCATTAAAGTATAAGCCTAACTTTGTGCTAGTCTCAAGGAGAAACCTTTAACCACAAG  
TTTTTATCATTGAAGACAATATTGAAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTTCAC  
TAACCCCTGACATACTCCCCACCCAGTTGATGGCTTCCCGTAATAAAAAGATTGGGATT  
TCCTTTTG

## **FIGURE 76**

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVRKLPPPLCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYN  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTQQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

### **Signal sequence:**

amino acids 1-48

### **Transmembrane domain:**

amino acids 111-125

### **N-glycosylation site.**

amino acids 165-169, 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

### **N-myristoylation site.**

amino acids 188-194, 225-231

### **Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

**FIGURE 77**[illegible]

## **FIGURE 78**

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPQPCGGPGLAPGVRSYGPR  
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGGSVRYPVVHPHPNCGPEPGVRSFGFPDFQSRLYGVYCYRQH

### **Signal sequence:**

amino acids 1-17

### **Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

### **Tyrosine kinase phosphorylation site.**

amino acids 137-145

### **N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCCTGCTGC  
TTCTGTGTCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGACACAGGCGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACCGGAA  
CTTCAGTACGACCATGAGGCTTCTCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCGCTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGAC  
GGCGACGGCTGGGTGTCTGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA  
CATACGGGACTCGGTGAGCGCGGCCCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGG  
GTGGGAGGAGCTGCGCAAACGCCACCTATGGCCACTACGCGCCCGTGAAGAATTTTCATGAC  
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGCGGCTTTCCGGTGGC  
CGACCAGGATGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCTGCAACCCGAGG  
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCTTGAGGACCTGGACAGAAACAA  
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA  
GGAGCCGCGGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGG  
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACCAGCCC  
CTGGTGGAAGCCAAACCACTGTGCAAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA  
AGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGCGGAGG  
ACCTGACCCGGCACACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGCCCG  
CACAATGACCGGAGGAGGGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGACAGGAG  
GCAGATGCAGTCCCAGGCATCCTCTGCCCTGGGCTCTCAGGGACCCCTGGGTGCGCTTC  
TGTCCCTGTACACCCCCAACCCAGGGAGGGGCTGTCTAGTCCCAGAGGATAAGCAATAC  
CTATTCTGACTGAGTCTCCAGCCAGACCCAGGGACCCCTGGCCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCCT  
GGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGAGGCAATAA  
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 80**

MMWRPSVLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKFDQLTPESQARLGRIVDRMDRAGDGDGWSLAE LRAWIAHTQQRHIRDSVSAAWDT  
YDTRDRGVRGWEEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ  
FRDFRDLNKGHLDGSEVGHVWLPPAQDQPLVEANHLHESDTDKDGRLSKAETILGNWNMFV  
GSQATNYGEDLTRHHDEL

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 140-144

### **Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

### **N-myristoylation site.**

amino acids 263-269, 311-317

### **Endoplasmic reticulum targeting sequence.**

amino acids 325-330



## FIGURE 81

GGGGCCTTGCCCTTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
 GCGGCGGGCGCGGTGCGAGGGATCCCTGACGCCCTCTGTCCCTGTTTCTTTGTGCGCTCCAG  
 CCTGTCTGTGTCGTTTGGCGCCCCGCCCTCCCGCGGTGCGAGGTGACACCGATCCTG  
 GGCTTCGCTCGATTGCGCGCCGAGGCGCCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG  
 CGGGTCGTCTGTGTCCTCTCTCCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGC GGGGCTCT  
 GAGGAGGTGACGCGCGGGGCCCTCCCGCACCTTGGCCTTGCCCGCACTTCTCCCTCTCTCCAG  
 GTGTGAGCAGCCTATCAGTCACCATGTCCGCGAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG  
 TGTCTGCTGCTGCTGCGGGGGCCGCGGGGCGAGGGAGCGCGCTCCCATTTGCTATACATG  
 TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGGCTGCC  
 CTCTTGAGGAATTTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG  
 GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC  
 TGGTCGAGAAAACATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAAATGCTTCTAGAT  
 GGTCTGCTTCTTTACAGTAACATAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
 GTGTCCACAGCACATCCACCAACAGGTAACGACTAAAGAAAACACCCGAGAAGAAAACCTGG  
 CAATAAAGATTGTAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC  
 GCCGATTTAATTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA  
 GAAGGACCACTGTGGGCCCTTGTTCAGGCCAGTGAACATCCAAAAATAGAATTTTACTTTGAA  
 AAACTTTACATCAGCCAAAGATGTTTTGTTTGGCATAAAGGAAGTAGGTTTCAGAGGGGGTA  
 ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAAATTCCTCACGGTAGATGCTGGA  
 GTAAGAAAAGGGATCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT  
 CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA  
 AGCCTATCCTTGAGAACTGGGGATGGTTCAGGATGTACATTTGTTGACAAGGCTGTCTGT  
 CGGAATAATGGCTTCTTCTCTTACCACATGCCCAAACCTGGTTTGGCACCACAAAATACGTAAA  
 GCCTCTGGTACAGAAGCTGTGCACCTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT  
 CAGTGAACATTGCTTTCTAATTTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCCTC  
 ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTGAAATCTCGGACATTTGGTGCCAAGAT  
 AGCTGCTGTACAGTTTACTTTATGATCAGCGCAGCGAGTTTCAAGTTTCACTGACTATAGCACA  
 AAGAGAATGTCCTAGCTGTCTATCAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT  
 GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAAGAA  
 CTTCTTAGTAATTGTACAGATGGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
 CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG  
 AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTTTCACAAGAGAGTTCACAGGATT  
 AGAACCAATTGTTTCTGATGTCATCAGAGGCATTGTAGAGATTTCTTAGAATCCCAGCAAT  
 AATGGTAACATTTTGACAACCTGAAAGAAAAGTACAAGGGGATCCAGTGTGTAATTTGATT  
 CTCATAAATACTGAAATGCTTTAGCATACTAGAAATCAGATACAAAACATTAAGTATGTGTAAC  
 AGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT  
 ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA  
 GATAATGTGGATTAAACCTTAAGAGTTCTAACCATGCCTACTACTACAGATATGCAAA  
 TTCCATAGCTCAATAAAGAATCTGATACTTAGACCAAAAAAAAAA

## **FIGURE 82**

MSAAWIPALGLGVCLLLLPGFAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEFSVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFATKEVGFRRGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLC THEQMMCSKTCYNSVNIAFLI  
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPKNFLVIVTDGQSYDDVQGPAAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

### **Signal sequence:**

amino acids 1-24

### **N-glycosylation site.**

amino acids 100-104, 221-225

### **Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

### **N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

### **Amidation site.**

amino acids 145-149

## FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCGAGCC  
GGCGGCCTCCCGCGGGAGCGAGCAGATCCAGTCCGCGCCCGCAGCGCAACTCGGTCCAGTGC  
GGCGCGCGGTTCGCGGCGCAGAGCGGAGATGTCAGCGGCTTGGGGCCACCTGTCTGTGCTGC  
TGCTGGCGCGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGTCCAGTTC  
AAGCCCGGCGCGGTCTCAGTACCCGAGGAGGAGGCCACCTCAATGAGATGTTCCGCGA  
GGTTTGAGGAATGATGGAGGACACGACGACAAATTCGCGAGCGCGGTGGAAGAGATGGAGG  
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACTTACCTCCAGCTAT  
CACAATGAGACCAACACAGACACGAAGGTTGGAATAATACCATCCATGTGCACCGAGAAAT  
TCACAAGATAACCAACACAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCATATCTG  
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC  
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT  
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCCAAA  
TGGCCACCAGGGGCGAGCAATGGGACCATCTGTGACAAACAGAGGGACTGCCAGCCGGGGCTG  
TGCTGTGCCTTCCAGAGAGGCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA  
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAGCTGGAGCTAGAGCCTGATG  
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCTCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAGCCGACCTTCGTGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC  
CAGAGAGTTCGCCGATGAGTATGAAGTTGGCAGCTTCATGGAGAGGTCGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCGCT  
GCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA  
ATAGCTAATTTATTTCCCGAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCTCTACA  
TCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTTTCAGC  
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGTCTGGGAGAGTACAGGCAGGGTTAAAC  
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACAGTTGGCAG  
ACAGCCGTTTGTCTCATATGGCTTTGATAATTGTTTGAAGGGAGGAGATGGAACAAATGTGG  
AGTCTCCTCTGATTGGTTTTTGGGAAATGTGGAGAAGAGTGCCTGCTTTGCAAACTCA  
CCTGGCAAAATGCAACAAATGAATTTTCCACGAGTCTTTCATGGGCACTAGGTAAAGCTG  
TGCTTTCAGCTGTTGCAGATGAAATGTTCTGTTTACCCTGCATTACATGTGTTTATTCATCC  
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC  
CCTCTCTCAGCACAGCCTGGGAGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAG  
GCTCAGAGACTCAAGCTGCTTGCCCAAGTCAACAGCTAGTGAAGACCAGAGCAGTTTCAT  
TCTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACAGCCTTGGTGCCACCAA  
AAGTGCTCCCCAAAAGGAAGGAGAAATGGGATTTTCTTGAGGCATGCACATCTGGAATTAAG  
GTCAAACATAATTTCTCACATCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTCTTCCAC  
AGTGTGGGCGAGCCGCTCTTCAATGAAGACAATGATATTGACACTGCTCTTCTTGGCAGT  
TGCTATTAGTAACTTTGAAGGTATATGACTGAGCGTAGCATACAGGTTAACTCTGCAGAAACA  
GTACTTAGGTAATTTGATGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC  
TGAAGACAATTTCAACCACTGGAGAGAAATCAAACCGAGCAGGCTGTGTGAACCATGGTT  
GTAATATTGCGACTGCAACACTGAACCTACGCCACTCCACAAATGATGTTTTCAGGTGTCA  
TGACTGTGTGTCACCATGTATTTCATCCAGAGTTCTTAAAGTTTAAAGTTGTGCACATGATTGTA  
TAAGCATGCTTTCTTGTAGTTTAAATTTATGTATAAACATAAGTTGCATTTAGAAATCAAGC  
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYQBEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEBAKASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTG  
QMVFSSETVITSVGDEEGRRSHBCIIDEDCGPSMYCQFASFQYTCQPCRQQRMLCTRDSECCG  
DQLCVWGHCTKMATRGSGNTICDNQRDCQPLCCAFQRGLLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEET

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### **N-myristoylation site.**

amino acids 202-208, 217-223

### **Amidation site.**

amino acids 140-144

## FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACAATCTCTCTGGGCTCAGAAAGGACTCTG  
 AAGATAACAAATATTTACGGCCATCCACTCTCTCCCTCCCAACACACATGTGTGATGTACACACACATACAC  
 CACACATACACCTTCTCTCTCTCACTGAAGACTCAGAGTCACTCACTCTGTGAGCAGGTCTATAGAAAAGGACAC  
 TAAAGCCTTAAGGACAGGCTGGCCATTACCTCTGCAGCTCTCTTTGGCTTGTGTAGTCAAAAACATCTGGGAGGGG  
 CCAGGCAACGGTGACTCACACCTGTATCCAGCATTTTGGGAGACCGAGGTGAGCAGATCTTGAGGTCAAGAG  
 TTCAGACCCAGCTGTGGCCACATGGAGAAACCCCATCTCTATAAAATACAAAATTAGCCAGGAGTGGTGCC  
 AGGTGGCTGTAAATCCAGCTACTCAGGTGGCTGAGCCAGGAGAAATCGCTTGAATCCAGGAGGCGGAGGTGCACT  
 CAGCTGAGTGCACCGCTGCATCTCAGCTCTGGGTGACAGAATGAGACTCTGTCTCAACAACAAACACCGGAGGA  
 GGGGTAGATATCTCTCTGTGCAACCTCTTAACTCTGCATCTCTCTCTCAGGGCTGCCCTGTATGGGGCTTG  
 GCAATGACTGAGCAGGCGCCAGCCCCAGAGGACAAGGAAGAGAGGCAATATTGAGGAGGGCAAGAAAGTGACGCCCG  
 GTGTAGAAATGACTGCCCTGGGAGGTGGTTCTTGGGCCCTGGCAGGGTTGCTGACCTTTACCTTGCAAAACACA  
 AAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCTGCCCTGCAGCTCCACATGAGGCTTCTCGTGGCCCC  
 ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCGTGGTACCCCTGGCATGTTCCCTGCCCCCCCTCA  
 GTGTGCCCTGCCAGATCCGGCCCTGGTATACGCCCCCGCTCGTCTACCGCGAGGCTACCACTGTGAGCTGCAATGA  
 CCTATTCTTGACCGGAGTCCCCCGGCACTCCCCGAGGCACACAGACCTGTCTGTGAGAGCAACAGCATTTGT  
 CCGTGTGGACAGAGTGAAGTGGGCTACCTGGCCAACTCTACAGAGCTGGACCTGTCTCCAGAAAGCACTTTTCGGA  
 TGCCCGAGACTGTGATTTCCATGCCCTGCCCAGCTGTGAGCTGTCACTAGAGGAGAAACAGCTGACCCCGCT  
 GGAGAGCCACAGCTTTTGCGGCTGTGGCAGCTTACAGGAATCTATCTCAACCAACACAGCTCTACCGCATCGC  
 CCCCAGGGCTTTTCTGGCTCAGCAACTGTCTGGGCTGCACTCAACTCAACTCTCTGTAGGGCCATTGACAG  
 CCGCTGGTTTGAATGCTGCCCAACTTGGAGATATCTCATGATTGGCGGCAACAGGTAGATGCCATCTGGACAT  
 GAATCTTCGGGCCCTGGCCAACTGCTGAGCTGGTGTGCTAGCAGGATGAACCTGGCGGAGATCTCGAGCTATGC  
 CCTGGAGGGGCTGCAAGCCTGGAGAGCCTCTCTTCTATGACAACAGCTGGCCCGGGTGCACAGGCGGGCACT  
 GGAACAGGTGCCCGGCTCAAGTCTCTAGACCTCAACAAGAACCCGCTCAGCGGTGAGGGCGGGGCACTTTGC  
 CAACATGCTGCCACCTTAAGAGACTGGGACTGAACAACATGAGGAGCTGTCTCTCATGACAACTTTGCCCTGGT  
 GAACCTCCCCGAGCTGAACAAGCTGACACCAATAAACCCACGGCTGTCTTCTATCAACCCCGGCTCTCA  
 CCACCTGCCCCAGATGGAGAGACTGATCTGCTCAACAACAACGCTCTCAGTGTCTGTGACAGCAGAGCGGTGAGTC  
 CTGCGCCCACTCTCAGGAGGAGTGTCTTCCACGGCAACCCCATCCGCTGTGACTGTGATCCGCTGGGCCAATGC  
 CACGGGCAACCGCTGTCTGCTCTCAGAGCCGCAATCAACCTGTGTGGCGAGCTCTGCGACCTCCAGCGCTCTCC  
 GGTCCAGTGGGTGCCCTTCCAGGATGACGAGCACTGTTTGCCCTCATCTCCCCCAAGAGCTTCCCCCAAG  
 CCTCAAGTACAGTGGAGAGAGCATGTGTGCTGCACTTGGCGGCACTGGCCGAAACCGAACCAGATCTACTG  
 GGTCACTCAGCTGGCTTCTGCTGACCTGCTGCCATGCAAGGAGGAGGTACCGGGTGTACCCGAGGGGACCTT  
 GAGCTGCCGAGGTTGACAGACAGAGAGGCAAGGCTATACACTGTGTGGCCAGAACTGGTGGGGCTGACAC  
 TAAAGCGTTAGTGTGTTTGGGCGGTGCTCTCTCTCAGCAGGCGAGGACGAGGACAGGCGGTGGAGCTCCG  
 GGTGAGAGGACCAACCCCTATCAGCATCTGTCTATCTTGGGTCAACCCCAACACAGTGTCAACCAACTCAC  
 CTGTGTCAGTGCCTCTCTCCCTCCGGGCGAGGGGGCCACAGCTCTGGCCCGCTGTCTCGGGAAACCCACAGCTA  
 CAACATTACCCGCTCTCTCAGGCCACGAGTACTTGGGCTGTCTGCAAGTGGCCCTTTGCTGATGGCCACACCCA  
 GTTGGCTGTGTATGGGCGAGGACAAGAGGCCACTTCTTGCCACAAGCTTTAGGGGATCGTCTGGGCTCAT  
 TGGCATCTTGGCTCTCGCTGTCTTCTCTTGGCAGCTGGGCTAGCGGCCACTTGGCACAGGCCAACCCAGGAA  
 GGGTGTGGGTGGGAGGCGGCTCTCCCTCAGCCTGGGCTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTTGT  
 GTCGTCTCCCTCTGCTCTGCCCTGGAATCCAGGAGGAAAGCTGCCAGATGCTCAGAAAGGGAGACACTGTTGCC  
 ACCATTGTCTCAAAATTTCTGAAGCTCAGCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTTTACAAA  
 AGAGAAGCAGTCTGGGCGAGTGTCCCTGCCAGGAAGGGACATGGAACCAAGTCTTGAAGCTGTGGCAGCTGGG  
 CAGACAGATGGGGCTTTGTGGCCCTGGGGGTGCTTCTGAGCCTTGAAAAGTGTGCCCTTACCTCTTAGGGTCA  
 CCTCTCTGCCATTTCTGAGGAACATCTCCAAGGAACAGGAGGACTTGGCTAGAGGCTCTGCTGCCCTCTT  
 CTCTCTGCCAGAGGCTCTCTGGGCTGGCTTGGCTGTCCCTACCTGTGTCCCGGGCTGACCCCTTCTCTCTC  
 TCTTTCTGTACAGTCTCAGTTGGCTTGTCTTGTGCTCTGGGCAAGGCTGAAGAGGCTCACTCAATCTCAC  
 CTGGGGGGCTGCCCTCAATGTGGAGTGATGCCACGAGCAGATCTGAAGGACATTTGGGAGGAGGTGCCAGGAA  
 CGCTCATCTCAGCAGCTGGGCTCGGATTCGAAAGCTGACTTCTATAGGCAATTTGTACTCTTTGTGGAGAA  
 ATGTGTCACTCCCCCAACCCGATTCACTCTTTCTCTGTTTTGTAAAAATAAAAAATAATAACATAAA  
 AAAA

## **FIGURE 86**

MRLLVAPLLLA WAGATATVPVVPVHVPCPPQCACQIRPWYTPRSSYREATTVCNDLFLTA  
VPPALPAGTQTLLQLQSN SIVRVDQSELGYLANLTELDLSQNSFS DARD CDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLHNHQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAI LDMNFRPLANLRSVLAGMNLREISDYALEGLQSL SLSFYDNO  
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNL P  
ELTKLDITNNPRLSFIHPRAFHHLPQMETMLN NNA LSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRPIEPQSTLCAEPPDLQRLPVRREVPPREMTDHCPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYVWVTPAGLRLTPAHAGRRYRVVYPEGTLELRRVTAAEEAGLYT  
CVAQNLVGADTKTVSVVVGRALLQPRDEGQGLELRVQETHPHYHILLSWVTPPNTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVGGRRLPPAWAFWGW SAPSVRVV  
SAPLVLPWNPGRKLP RSSEGETLLPPLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

**FIGURE 87**

CTAACGACAGGGCGCGTCTTCAGAGAGGTGAAGAAGTCTCGGGACCATGTGGAGAGGGGGACATTTGTGTACCGCTT  
CTATATGCGGCAGACCATCTCAAGGTGATCAAGTTCACTTCATCTGCTACACCGCTCTACTAGCTGCACAA  
CATCAAGTTCAGCGTGCATCTGCACCTTGACATTTAGAGAGCCTGACGGGCTACCGCCTACACCGCTTGCGCCACCC  
CTCGGAGCTGCATCTTCAAGATCTCTGCGCTCTTCTCATTCAGCAGCTAGTCACTTCTTCACTGCGCTCATCTGCTATGA  
CAACATCTGTGTGATGCTCATGGCGCTCTCCCTCAAGAAGTACTCGTTTGATCGATCCGTGGAGGAGCAGCTACGAG  
CGACATCTCCGAGCTCAAGAAGCACTTCGCGTTTCATGCTGCACCTCATTCGACCAATACGACCGCGTCTACTCTCAA  
GCGCTTCGCGCTTCTCTCTCGAGGATGAGTGAAGAAGCTCTCGGCACTGTGAACCTCAACAGAGGTCGAGCGCT  
CGACAGAGCTCCGGCAGCGGCTCACCAGAAAGCGCGGAGCAAGCTGGAGCTGCACCTTCTTCATGCTCAGTGGAGCT  
CCCTGACACTGTGTTTGAAGCTGTGGAGCTCGAGGCTCTCAAGCTGGAGCTGCACCTCCCGAGCTGACCATCCGCG  
CAGCATTTGCCAGCTCACGGGCCTCAAGAGCTGTGGCTCTTACCACACAGCGGCCAAGATTGAAAGCGCTCGCG  
GCGCTTCTCGCGAGAACTCTCGGGCGCTGCATCACTAAGTTACCGACATCAAGAGGATTCGCGCTGTGGATCTTA  
TAGCTTGAAGAACACTGGAGAGGCTGCACCTGACGGGCAACTGAGCGCGGAGAAACACCGCTCATACGTATGTCATGA  
CGCGCTCGGGAGCTCAAAGCCTCAAGTGTCTCGGCTCAAGAGCACTTAAGCAGATCTGCCAGCTGGTGTCACT  
AGATGTGGGCGTGACATCTCGAAGCTGTTCATCAACAATGAGGGCAACAAGCTCATGTCCTCAACCTGCGCTCAA  
GAGATGTGGCAACTGACTGACTGAGCTGAGCTGATCCGCTGCACCTGGAGCGACTCCCCCACTCAATCTTCAAGCT  
CCACACACTTCGAGGAGATTGACTCTCAAGGACAAACAACCTCAAGACCATCGAGGAGATCATTCGCTCTCGACACT  
CGACGCGCTCACTGCTTTAAAGCTGTGTGACAAACCATCTCGCTTACTCCCTACCGATTCGGAACCTCAACAA  
CTCGGAGCGGCTCTACTTGAAGCGGACATGACTGAGAGATGCCACCACTGCTTCTTAACTCGCGCAAGTCTGCG  
CTACCTGGACCTCAGCACAACAACATGACTTCTCTCCGCACTCATGCGCTCCTGCGAGCTCTCAAGAACT  
AGGCTACACGGGCAACCGGGATGAGAGCTCTCCCTTCGGAAGTCTTTCAGCTCCGGAAGTCTGGGGCGCTGCACCT  
GGGACAAACGCTGTGCTCAGTCACTGCCCTTCAGGCTGGGCGACTCTGACCAACCTGACGAGATGAGCTCGGGG  
CAACCGCTGGAGTGTCTCTGCTGTGAGAGCTGGGCGAGTCCCACTCTGCAAGGCGACGGCTCTGTGTGGAGGA  
GGACTGTGTTCAACACTGCCACCGAGGTGAAGGCGGCTGTGAGGGCTGACAGAGGCTGAGGCTCGGCTGAAGGA  
CGCCGCGCAGACAGCAGCAGCAGCAGCGCTCGCCAGTCTCGAGGCGCGAGGGGACGGCTAGCTCTTCCGAC  
NACTCCCGGACGAGCAGACAGCTCGCGCTGGGCGAGAGCTCGGGCGCTTGTAGATGACGACAGCAGAGGAGA  
GGAAGATGCTGTGGGCTGTGCCCTTTCTTCCTCTGAGACTCAAGTCCCCAGGCAAGTCTGTGTGGAGGAG  
AGCAAGTCTCAAGAGCGAGTATTTGGAATCTAAGGCTCTCTCCCTGGAGGACAGCTCTGCCCAAGGGCTGAG  
CTGCCAACAGAGTCTGGGACCTCACTTAGTTCTTGATATTTATTTTCTGCATCTCCCACTCTCCCTTCCCT  
AGATAACTTATACATTTCCAGAAAGAACTTCAGCCAGATGAGAGTGTGAGGAAAGGTGGGCTGCTTTTCCCT  
TTGTCTTATTTAGCGATGCGCGCGGAGCTTAAACACCACTGGAATCTCAGCAGAGTGTGCGGGGGAACACG  
CAGTGGGACGGTCAACCGAGCTGCGGGCTGGGCTCTGCGGTGCGGTTCAGGAGAGGACAGGAGCTCTCAGCTGTG  
AAGGCGACCGCTGGAGCTTGCTCTTCAGTTTGTGGCAGTCTTGGATTTTGTGTTTTTTTTTTTTTAAATCAA  
AAACAATTTTTTTTTAAAAAAGAGTTTGAATAAGTATGGTTTGGGTATTAAGAAAGAAAAAACTTAAAAAA  
AAAGACCACTAATGGCGCATGAGTTGGAGTCTCAGGCGAGGGTGTGAGTTTCCCTTGAGAAAGACGAGCAGAGT  
TGAACCTGTGTTTTCTTTCTGGGCGAGGTTGAGGTTCTCCGAGATCTGGTGTGACCTTGTGCAGAGATTT  
CTATTTGTTCTCGGGAGGAGGAGTTTTTTTGTGTTTTTGGGTTTTTGGTGTCTTGTTTTCTTCTCTCTC  
ATGTTGCTTGGCAGCATCATTTTCTGTGGCTGTCCGCAAGAGGAATTTCTTGAGAGCTCAGAAAGGGAGGAG  
ACTCGAGTTGGCTAATCCCGGAGTGAAGCGGTGCTCATTCGCACTCCCTCTGCTGCTGCTGCTCTGCTCTCA  
CGCACAGTTTAAAGGACCAAGAGAGGACCATTCGCCAGACTTTGTTTCCCACCTCTCGGCTCGGSCATGGGTTGTGT  
CAGTGGCCACCGCTGGCTCTCGCTGCTCTCATCGACTCTGCCCACTGTCTTATGAAGAGCAGACACTTA  
GAGGCTGTGTGGGAATGGGAAGTGCCTCTCGGGAGGCGAGGCGTGGTTCAGGACCGGTTTCCCGTCTGGGCG  
CTGGAATGCACAACGCCAGTGGCGACTGCTGGTGTGAGGCAACCTGCTTTAGATCATCTGGGTCGCCCACT  
AGAAGGTTCCCGCGCTTAGATCAATCAGTGCAGCAATGAGCAGCTTTAGAGTCTGCTGTCTTAAATGATTATG  
CATCCGCTGTGCTGCTCATTTGTGTTTTGTTTCTGCGTGTGCTCATGTGATATACTCAGAAATATGACACATAG  
CCTCTGACCAACTGAAGCAAAAAATCCGTTACATGTGGTCTGAACTTGTAGACTCGGTCAACGATCAAAATAA  
ATCTATACAGCAAAAAAAAAA

## **FIGURE 88**

MRQTIKVIKIFILIICYTVVYVHNKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHLFMLSIGIPDTVFDLVELEV  
LKLELIPDVTIPPSIAQLTGKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWI  
YSLKTLLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKMANLLELELIRCDLERIPHSIFSLHNLQEIIDLKDNNLKTIEEIIISFQ  
HLHRLTCLKLWYNHAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKRLRALHLGNNVLQSLPSRVGELTNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

### **Transmembrane domain:**

amino acids 51-75 (type II)

### **N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

### **Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

### **N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447



## FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCA**TGG**GAGCTGGCACTGCGGCGCTCTCCCCT  
CCC GCGGTGGTGTCTGCTGCTGCCGCTGCTGCTGGGCTGAACGCAGGAGCTGTCA**TG**ACT  
GGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC**TAC**ATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGT**CA**T  
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATT**TG**GAAACTTTGAGGAAAT**TTGG**GC  
CCCTTGACAGTGATCTCAAACCACGAAACCACCTGGCTCCAGGCTGCCAGCTCTCTATTT  
GTGGATAATCCCCTGGGCACTGGGTTCA**GT**TATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCA**GT**TGCCACA**AA**G  
AATCCAGACAGTTCATTCTACATTTTCTCAGAGTCTATGGAGGAAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTTATAAGGCCATT**CAG**CGAGGGACCATCAAGTGCAACTTTGCGGGGGT  
TGCCTTGGGTGATTCTGGATCTCCCTGTTGATTCCGTGCTCTCCTGGGGACCTTACCTGT  
ACAGCATGTCTCTTCTCGAAGACAAAGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGGTGAACTTCTATAACATCTTAACTAAAGCACTCCCA  
CGTCTACAATGGAGT**CG**AGTCTAGAATT**CAC**ACAGAGCCACCTAGTTTGTCTTTGT**CAG**CGC  
CAGTGAGACACCTACAACGAGATGCC**TTA**AGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGCTCTTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGTCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGT**CAG**GAGGCCTG  
GGTGC**GAA**AACTGAAGTGCCAGA**ACT**GCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGT  
ACAGTGAC**CTA**AAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCT  
TACTGGATTCTGAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGACTCAGCAAGAA**TAG**GATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT  
TGGGGCAGAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTTGGAAATATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT  
TTGTTTTGATCAAAATAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLLPLLLGLNAGVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNGLYRE  
ATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESLEFQSHLVCLCQRHVRHLQRDAL  
QLMNGPIRKCLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWVRKLKWPPELPKFSQLKWKALYSDBKSLETSAPFKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

### **Signal sequence:**

amino acids 1-25

### **N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

### **Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

### **N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## FIGURE 91

GGCCGCGGGAGAGGAGGCC**ATG**GGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCGTTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACCTCGGGCGTTGGCCGTGGCA  
GGGAGCCTGCGCCTGTGGGATTCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTACCCCTATGACATTG  
CCTTGTTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG  
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTCAGGTCGCCATCATAAACA  
ACTCTATGTGCAACCACCTCTTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG  
GTTTGTGTGGCAACGCCCAAGGCGGGAAGGATGCCCTGCTTCGGTGACTCAGGTGGACCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG  
GTTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCCTTTGAGTGGATCCAGAAG  
CTGATGGCCAGAGTGGCATGTCCAGCCAGACCCCTCCTGGCCACTACTCTTTTTCCCTCT  
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCT**TGA**GCCTACCTGAGCCCATGCAGCCTGGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGGTAAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLLALLARAGLRKPESQEAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRW  
DSHVCVGSLLSHRWALTAACHFETYSDDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVITYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSSGGPLACNKNG  
LWYQIGVVSWGVCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

### **Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

### **N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

### **Amidation site.**

amino acids 33-37

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

### **Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT  
CTTTGCCCCATCCTCTCTGCGCAAAATGCAGTTACAGCCCCGGAGCCCGACCGGAGGACGC  
TGCCCCCAGGCTGGGTGTCCCTGGGCCGTGCGGACCTTGAGGAAGAGCTGAGTCTCACCTTT  
GCCCTGAGACAGCAGAAATGTGGAAGAAGTCTCGGAGCTGGTGCAGGCTGTGTGCGATCCAG  
CTCTCCTCAATACGGAAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC  
CACTGACCCTCCACACGGTGCAAAAAATGGCTCTTGGCAGCCGGAGCCAGAAAGTGCCATTCT  
GTGATCACACAGGACTTTCTGACTTGTCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC  
TGGGGCTGAGTTTCATCATTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCCCTTGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT  
TTTCCCCAACATCATCCTCTGAGGCAACGTCTCTGAGCCGAGGTGACAGGGACTGTAGGCCCT  
GCATCTGGGGGTAAACCCCTCTGTGATCCGTAAGCGATACAACCTTGACCTCACAAGACGTGG  
GCTCTGGCACCAAGCAATAACAGCCAAGCCTGTGCCAGTTCTCTGGAGCAGTATTTCCATGAC  
TCAGACCTGGCTCAGTTCTATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC  
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT  
ACCTGATGAGTGCTGGTGCCAAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG  
GGACAGGAGCCCTCTCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCTACATCCAGCGGGTCA  
ACACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCCCTGCTCTTCGCCCTCAGGTGACAGT  
GGGGCCGGGTGTGGTCTGTCTCTGGAAGACACCAAGTTCCGCCCTACCTTCCCTGCCCTCAG  
CCCCATGTGCACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCCCTCATCAAAATGAAA  
TTGTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACGGCCCTTCATACCAGGAG  
GAAGCTGTAAACGAAGTTCCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC  
CAGTGGCCGTGCTACCCAGATGTGGCTGCACCTTCTGATGGCTACTGGGTGGTCAGCAACA  
GAGTGCCCATTCATGGGTGTCCGGAACTCGGCCCTCTACTCCAGTGTTTGGGGGGATCCTA  
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTCTCAACCCAAAG  
GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAAACCGTGGCTCCATGAGTCTGTGC  
TGAGTGAAGAGGTGAGAGGCCAGGGTTTCTGTCTCTGGTCTGGCTGGGATCCTGTAAACAGC  
TGGGGAACACCAACTTCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCCCTATC  
AGGAGAGATGGCTTGCCCCCTGCCCTGAAGCTGGCAGTTTCACTCCCTTATTCTGCCCCGTG  
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA  
TGCTGTGAGCTTGACTTGACTCCCAACCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCTTAGATTCTCAATAAGATGCTGTAACTAGCATTTTTTGAATGCCTCTCCCTCCGC  
ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACATA  
TTTCACTTGATATTCATTTCCCAATTTCACTGCAAGGAGACCTCTACTGTCACCGTTTACTCT  
TTCTACCTGACATCCAGAAACAATGGCCCTCCAGTGCATACATCTTCTCAATCTTGTCTTATG  
GCCCTTCCATCATAGTTGCCCACTCCCTCTCCTTACTAGCTTCCAGGTCTTAACTTCTCTG  
ACTACTCTTGTCTTCTCTCTCATCAATTTCTGCTTCTTCAATGGAATGCTGACCTTCATTGC  
TCCATTTGTAGATTTTGTCTCTCTCAGTTTACTCATTTGCCCCCTGGAACAAATCACTGACA  
TCTACAACCATACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAA  
TGTAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQQCHSVITQDFLTCWL  
SIRQAEALLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLSAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPSSSYFNASGRAYPDVAALSDGYVWVSNRVPIPWVSGTSASTPVFGILSLINEHRILSG  
RPPLGLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSPGWDVPTGWGTPTSQLC

### **Signal sequence:**

amino acids 1-16

### **N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

### **Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

### **Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

### **N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## FIGURE 95

GC CGCGCTCTCTCCCGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC  
GGGTGCTCGGCGCGGAACAGTGTCTCGGCATGCGAGGGATTCCAGGGCTCCTCTTCTCTCTC  
TTCTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCACTTG  
GCCTGCATACCGCTCCCTGTCTGCTTTGCCCAAGTCTACCTTCAATTTAGCCAAGCCAGACT  
TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGGACCCAGTGTCATAAGGGAAC  
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG  
CAGCCGCACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC  
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC  
AGGTTCAGCATTTTTGGGAAGGACTTCTCTGCTCAACTACCTTTTCTCAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAAGCATGTCTCAGAGTGCCCCACTGCA  
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCTTAAAGCCC  
AAGTTTAAAGATGGTGGTTCGAGGGGCCAACGACTCCACTTCAGCCATGCCCCAGCAGATGAA  
ATTTTCAGTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTAAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGGTGAGCCCTCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACCTTCTC  
TGGTTATGACAATGACCGACCAGGCAATTTGGTGTATCGTTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGCTCTACAGCAATGCGATGCCCAGCCAGGGGCCAGCGGGTCTGGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTTCAGG  
GCACCAGTGGGTGGACATGAATGGTTCCCCACAGGATTTCAACGTGGCTGTGCAATCACTC  
CTCTCAAATATGCCCAGATTTGCTATTGGATTAAAGGAACTACCTGGATTGTAGGGAGGGG  
TGCACAGTGTTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTTTAGGAGAGGCC  
AAATGTTTTTTGTCTATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTGTGTAAAGGTGT  
CTTATAATCTTTTACCTATTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAACTG  
GTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATACTTTTGCATAGAAATAA  
AAAAAATACTGATTTGGGGCAATGAGGAATATTTGACAATTAAGTTAATCTTCACGTTTTTG  
CAAACCTTGATTTTTATTTCATCTGAACCTGTTTCAAAGATTTATATTAATATTTGGCATA  
CAAGAGATATGAAAAAAAAAAAAA

## **FIGURE 96**

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS  
RRKRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG  
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA  
LLELKPKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD  
AQPGASGSGVYVRMWRQOQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW  
IKGNYLDCREG

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 93-97, 207-211

### **Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

### **Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

### **N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

### **Serine proteases, trypsin family, histidine active site.**

amino acids 171-177



## FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCCGCCCCACCAGCCATGGTGTTT  
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGCGGCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC  
ACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGGAACCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCTGTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC  
CCCACCTCAGACCTGCGAGAAGCTGAAGGTTCCCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCTTGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC  
GGGGTCTACATCAGCCTCTCTGCGCACCCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA  
GCTCCGCGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG  
CCGCGCGCTCTAGGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGCGCGGCAGATCCACA  
TCTGGATCTGGATCTGCGGCGGCCCTCGGGCGGTTTCCCCGCCCCGTAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCCCCAC  
GACTTCCGGCCCCGCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTAT  
AGGTATTGTAAACCTGCCACATATCTATTATTCTCCAATTTCATAAATTATTTATT  
CTCCAAAAAAAAA

## **FIGURE 98**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFSTLLLLASTAILNAARI PVPPACGK PQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITA AHCFKDNLNKPYLFSVLLGAWQLGNPGSR SQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSEVLPICLPDAS IHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWGEGBAERNRPGVYISLSAHSR SWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

### **Signal sequence:**

amino acids 1-32

### **N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### **Glycosaminoglycan attachment site.**

amino acids 826-830

### **Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### **Tyrosine kinase phosphorylation site.**

amino acids 607-615

### **N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCGCCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGGCCAC  
AACAAGGAGCGCGGGCGCGCGGCGAGAATCTGTTCCGCATCAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT  
GCAGCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC  
GGCTGTGGTTCCTCACTTCTGTGAGAAGCTCCAGGTGTTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGGAACTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC  
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTGCTTACCTGGTAAGTGAAGGGCCATCCTTCCGGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT  
TGTTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAACCCAGGCC  
CCAACCTTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC  
AAGTGAAGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCAGAGAATCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG  
GGAATCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG  
AGGTCTTGGCCTCAGTTTTTCCAGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA  
AGCCTAGCGTTGTGTCAAGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA  
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTCTTGAATGGGATACCACTCAAAGGG  
TGAAGAGGTGAGCTGTCTCCTGTATCTTCCCCACCTGTCCCGACGCCCTAAACAAGATA  
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC  
ATCTTGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC  
GGGCCCCACCTCTCCTGCCCTCCTCCTGTAGTCTGGGGGTGGGAGGATTTGAGGGAGCT  
GAGTGCTTACCTGGCCTGGGGTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG  
TGTAAGTGGGGATGGGGATTCTTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC  
TTTGAGTGGGGGAGGACAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFLMLLLPLLLLLLVATTGPGVGTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEE  
LAAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLGVEETNIELLCNYPEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTPTSSLATGIPAFVLVTEV  
SGSLATKALPAVETQAPTSLATKDPSPMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEAEELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSV  
SGLNSGPGHVWGPLLGLLLLPLVLGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

# FIGURE 101

GTAAC TGAAGTCAGGCTTTTCATTGGGAAGCCCCCTCAACAGAAATTCGGTCATTCTCCAAGTTAT**TAT**GTGGACGT  
 ACTTCTGTTGTTCTCCCTCGCTTGCTTTTTACATTAGCAGACCGGACTTAAAGTACAACAGATTATCTTTTCAT  
 CAAGGCAAGTTCATCATTGAGCACCTTTCAAAGCCTTCGAGAAGTGAACTGAACACAAATGAATTTGGAGACCATTC  
 AAATCTGGGACGAGCTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTTGGAAATACCTCCCTGA  
 ACATCTGAAAGAGTTTCAGTCCCTTTGAAACTTTGGACCTTAGCAGCAACAATTTTCAGAGCTCCAAACTGCATT  
 TTCAGCCCTCAGCTCAAAATATCTGTATCTCAACAGCAACCGAGTCAAGTCAATGGAACCTGGGTATTTTGACAA  
 TTTGGGCCAACACCTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGATATCCACCCAAAGTCTTTTAAACT  
 GCCCAACTGCAACATCTCGAATTTGAACCGAAACAGATTTAAAAATGTAGATGGAGTGCATTTCCAGGCCCTTGG  
 TGTCTTGAAGTCTCTGAACTCAGCAAAATGCCATCAACAGGATCAGCCCTGATGGCTGGGAGTCTTTGGGGCTGAGCAA  
 CATGGAATTTTTCAGCTGGACCAATAACACTTAACAGAGATTACCAAAGGCTGGCTTTTCAGGCTTGTGATGTCTG  
 GCGAAGACTTCACTCTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGGCTTCGGGGCTTCCGCCAAGCTCAG  
 TGAGCTGGACCTTAACCTTCAATCACTTATCAAGGTTAGATGATTCAGCTTCTCTGGCCTAAGCTTAACTAAATAC  
 ACTGCACATTTGGGAACAACAGAGTCAGCTACATTTGCTGATTTGCGCTTCGGGGCTTTTCAGTTTAAAGACTTT  
 GGAATCTGAAGAACAAATGAAATTTCTCGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTGAG  
 GCGACTGATACCTCAAGGAAATCGGATTCGTTCTATTACTATAAAAGGCTTCACTGGTTTGGATGCAATTTGAGCA  
 TCTAGAGCTGAGTGACACGCAATCATGTCTTTACAAAGCAATGCATTTTCACAAATGAAGAACTGCAACAAT  
 GCAITTTAAATACATCAAGCTTTTGTGCGATTGCGAGCTAAATGGCTCCCAAGTGGTGGCGGAAACCACTT  
 TCAGAGCTTTGTAAATCCAGTTTGTGCCATCTCAGCTGCTAAAGGAAGAACATTTTGTGTTATGCCCAGA  
 TGGCTTTGTGTGTGATGATTTTTCGCAAAACCCAGATCACGGTTGAGCCAGAACACAGTCCGGCAATAAAGGTTTC  
 CAATTTGAGTGTTCATCTGCTCAGCTGCGAGCGAGTGATTTCCCAAATGACTTTTGTCTGGAAAAAGACCAATGA  
 TACTACTGCATGATGCTGAAATGGAAAAATATGCAACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCCAC  
 CATCTCTTCCGCTCGCGGAGGTGGAATTTTGGCAGTTGCGAGCTAAATGGCTCCCAAGTGGTGGCGGAAACCACTT  
 ATCCTACTCTGTCAAAGCCAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCATGGATCTCAGCAT  
 CCGAGCTGGGGCATGGACGCTTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCAGATAGCTGGCAGAGGA  
 TGGGGGACAGACTTCCAGCTGCAAGGGAGAGACGATGCATGTGATGCGCCAGGATGACGTGTTCTTTATCGT  
 GGATGTGAAGATAGAGGACATTTGGGATATACAGCTGCAACAGCTCAGAAACAGTGCAGGAAGTATTTTCAGCAAAATGC  
 AACTCTGACTGCTCTAGAAACACCATCATTTTTCGGGCCACTGTTGGACCGAAGCTTAACCAAGGGAGAGAACAGC  
 CGTCTCAAGTGCATTTGCTGGAGGAAGCCCTCCCTTAAACTGAACGGACAAAGTATGATAGCCCATTTGGTGGT  
 AACGAGAGGCACTTTTTCGAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAAGTGTGCTGGGAA  
 ATACACATGTGAGATGTCTAACCCCTTTGCGACTGAGAGAGGAAACGTCGCTCAGTGTGATCCCACTTCCAAAC  
 CTGCGACTCCCTCAGATGACAGCCCATCGTTAGACGATGACGGAATGGGCCACTGTGGGTGCTGATCATAGC  
 CGTGGTTTGTGCTGTGTGGGACGTCACCTGTTGGGTGCTCATCATATACCAACAAGGCGAGGAATGAAGA  
 TTGCACTTACCAACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTTGTATCTCAGGGAACGTT  
 AGCTGACAGGCGAGGTGGGTACGTCCTTCAGAAAGTGAAGGCCACCAAGCTTTGTGCATCTTCAGGTGCTGG  
 ATTTTCTTACCAACAATGACAGTGTGGGACCTGCCATATTGACAAATAGCAGTGAAGCTGATGTGGAAGCTGC  
 CACAGATCTGTTCTCTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTTATTTGAAGGGAATGTGATGCTCAGA  
 TCCCTTTTGAACATATCATACAGGTGCGACTCTGACCCAGAAACAGTTTAAATGGAACCATATGAGCCAGTTA  
 CATAAAGAAAAAGGAGTGTACCTACCTTTTCTCATCTTCAGAAAGTCTGCGGAGCGGAGCTTCAGTAAATATC  
 GTGGCCTTCAATGTGAGGAAGCTACTTAACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTG  
 TCTAAACAGCTCTCTTTAGATTTTAGTGCAAAATCCAGAGCCAGGCTGCGTTGCCCTGAGTAACTTTCTTCATGGG  
 TACCTTTGGAAAGCTCTCAGGAGACCTCACTAGATGCCATTCAAGCTTTGGACAGCCATCAGATTGTGAGCC  
 AAGAGCTCTTTATTTGAAGCTCATTTCTCCCAAGCTTTGACTCTGGGTGAGGAAGATGGGAAGAAAGGAC  
 AGATTTTCAGGAAGAAATTCATTTGTACTTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTTCAGTC  
 TTATGCTTTGACACAT**TAG**ACTGAATGAGACCAAAGGAAAGCTTAACTACTACTCTCAAGTGAACCTTTTATTTA  
 AAGAGAGAGAACTCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAATCTGTTTATTCACAGAT  
 GAACAAAATTAACAAAGTTATGAAAAATTTTATACAGTGGAAATGATGCTCATATGAATATACCTTTTAAACTA  
 TTTTAACTTTGTTTATTCGAAAAAGTATCTACGTAAATTAATGATATAATCATGATTTTATGTATTT  
 TTATAATGCCAGATTTCTTTTATGAAAAATGAGTTACTAAAGCATTTTAAATACTACGTCTTGTACCATTTT  
 TTAATAGAAAGTACTTCTATTATATTTTGCACATTATATTAAATAAAGTGGTCAATTTGAA

## FIGURE 102

MVDVLLFLSLCLLFHISRDPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLILNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPLQLHLELNRRNKIKNV DGLTFQGLGALKSLKM  
QRNGVTKLMDGAFWGLSNMEILQLDHNNTLETITKGWLYGLLMLQELHLHSQNAINRISPDWE  
FCQKLSLELDLTFNHL SRLDDSSFLGLSLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNE  
ISWTIEDMNGAFSGLDKLRRLILQGNRI RSITKKAFTGLDALEHLDSLDAIMSLQGNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWL PQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNDLHDAEMENYAH LRAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKT PMDLTIRAGA  
MARLECAAVGH PAPIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN  
SAGSISANATLTVLETPSFLRPLLDRTVTTKGETAVLQCIAGGSPPPKLNWTKDDSP LVVTER  
HFFAAGNQLLIIVDSVSDAGKYTCMSNTLTGERGNVRLSVIPTPTCDS PQMTAPSLDDDG  
WATVG VVI IAVVCCVGTSLVWVVI IYHTRRRNEDCSI TNDETNLPADIPSYLSSQGT LAD  
RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSADVEAATDLFLCPFLGSTGP  
MYLKGNVYGSDDPPEYHTGCSDDPRTVLMDHYEPSYIKKKECYPCSHPSEESERSFSN ISW  
PSHVRKLLNTSYSHNEGPGMKNCLNKSSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFQPSDCQPRAFYLKAHSSPDLDSGSEEDGKERTDFQEENHICTFKQTL ENYRTPNFQS  
YDLDLT

**Signal sequence:**

amino acids 1-19

**Transmembrane domain:**

amino acids 746-765

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,

628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,

314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,

671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,

1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,

612-618, 623-629, 714-720, 873-879

# FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCTTGCAAAAATG  
AAGATGTCAGGACCGCAGCTTTCTCTGGAAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTTTCTGTGAGCCCTGGATCTTAAACAAAATGTGTATATGTGCACACAGGAGCATTCAAGAAATGAAA  
TAAACAGAGTTAGACCCCGGGGGTGTGGTGTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCTCCCTCC  
CCACCCCAAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCACAAAGAAAAAGTATGTTTCATTTTTCTC  
TATAAAGGAGAAAGTGAGCCAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAACT  
GGTGTGGTGGTGTTCCTTTTTCTTTTTGAATTTCCCAAGAGGAGGAAATTAATAATACATCTCGCAAAAGAAA  
TTTCAGAGAAGAAAAGTGACCGCGGAGATTGAGGCATTGATTGGGGGAGAGAAACCGACGAGCAAGTGGGA  
TTTGTGCCTTATGTTGACTAAAATGACGGATAATTGCAAGTTGGAATTTTCTTCATCAACCTCCTTTTTTAAAT  
TTTTATCTCTTTGGTATCAAGATCATGCGTTTTCTCTGTCTTAAACCACTGGATTTCATCTGGATGTGCT  
GTGATCAGTCTGAAATACAACTGTTTGAATTCAGAAGGACCAACACAGATAAATTATGAAATGTTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGCTCTAGGTTTAAACAGGGCCCTATTGACCCCTGCTTGTGGTGTCT  
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA  
CCAGTTGAGCAAGGTGATTGTGTTGCGAAAAACCTGCGTGAGGTTCCGGAATGGCATCTCCACCAACACACGGCT  
GCTGAACCTCCATGAGAACCAATCCAGATCATCAAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAATCTCT  
ACAGTTGAGTAGGAACCATATCAGAACCATGAAATTTGGGGCTTCAATGGTCTGGCGAACCTCAACATCTTGGA  
ACTCTTTGACAACTGCTTATACCACTCCGAATGGAGCTTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTT  
CGGAAACAACCCCATGGAAGCATCCCTCTTATGCTTTTAAACAGATTTCTCTTTGCGCCGACTAGACTTAGG  
GGAATTGAAAAGACTTTTACATCTCAGAAGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTGAACTTTGC  
CATGTGCAACCTTCGGGAATCCCTTAACCTCACACCGCTCATAAAACCTAGATGAGCTGGATCTTTCTGGGAATCA  
TTTATCTGCTCATCAGGCCTGGCTCTTTCCAGGCTTGTAGTCACCTTCAAAAACCTGTTGATGATACAGTCCCAGAT  
TCAAGTGTATGAAACGGAATGCCCTTTGCAACCTTCAGTCACTAGTGGAGATCAACTGGAGCAATAATCTTAAC  
ATTACTGCTCATGACCTCTTCACTCCCTTGCACTCATAGAGCGGATACATTTATCATCACACCTTTGGAAGTG  
TAACTGTGACATACATCTGTGGCTCAGCTGGTGGATAAAAGCATGGCCCTCGAACACAGCTTGTGTGCGCCGGT  
TAAACATCTCCTCCCAATCTAAAGGGGAGGTACATTTGGAGAGCTGAGCAGAAATACTTTCATATGCTATGCTCGGT  
GATTTGGGAGGCCCTGACAGCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGCGGCCCTCCACATC  
CCTGACATCTGTATCTTGGATTATCTCAAAATGGAACAGTGCATGACACATGTTGGGCGGTACAAAGTGGGATAGCTGT  
GCTCAGTGATGGTAGCTTAAATTTCACAAATGTAACTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA  
TTCCGTGGGAATACTACTGCTTCAGCCACCTGAAATGTTACTGCAAGCAACCACTACTCCTTTCTCTTACTTTTC  
AACCCTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCAAGATACCAATGTGGGTCCCCTCC  
AGTGGTCACTGGGAGACCAACCAATGTGACCACTCTCTCACACCAAGAGCAAGGTCGACAGAGAAAACTCT  
CACCATCCCAGTGACTGATATAAACAGTGGGATCCAGGAATTGATGAGGTGATGAAGACTTCAAAAATCATCAT  
TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAAGTATGCTGGTCATTTTCTACAAAGATGAGGAAGCAGCACA  
TCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTAATTAATGTGGATGATGAGATTACGGGAGACACAC  
CATGGAAGGCCACTCGCCATGCTGCTATCGAGCATGAGCACCTAATCACTATACTCATACAAATCTCCCTT  
CAACCACACAAACAGTTTAAACAAATAAAATTAATAACAGATTCAAGTCAAGACCGTTATTGATCCGAATGAA  
CTCTAAAGACATGTACAAGAGACTCAAAATCTAAACATTACAGAGTTACAAAAAACAAACAAATCAAAAAA  
GACAGTTTATTAATAATGACAAATGATGGGCTAAATCTACTGTTTCAAAAAATGTCTTTTCAAAAAA  
AAAAGAAAAGAAATTTATTTATTAATAATCTATTGTGATCTAAGCAGACAAAA

## **FIGURE 104**

MLNKMTLHPQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVDPGISTNTRLLNLHENQIQIIKVNSEFKHLRHLLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLLTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDLDELDSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHPWNCNCDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
LKCRASLTSVSWITPNGTVMTHGAYKVRIAVLSDGTNLNFTNVTVQDGTMYTCMVNSVGN  
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTDNNVGPTPVVDWETTNTVTTSLTPQ  
STRSTEKFTTIPVTDINSGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN  
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHNYSYKSPFNHTTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537



# FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCACTTGGCAGTTTGGCAGTTTCTTTTCGTTTCCCTCCTGCTGTTTGGGGGGCA  
TGAAGGGCTTCGCGCCCGGAGTAAAGAAAGGAATTTGACCGGGCAGCGCGAGGAGGAGCGCGCACCGACCGC  
GAGGCGCGCGCTGCACCTTCGGCTGGAAGTTTGTCCGGGCGCCGAGCGCGCGCTTCGGGAGCTTCGGGTAGA  
GACCTAGGCGCGTGCACCGCGATGAGCGCGCGCGAGCCTCCGTGCGCGCGCGCGCGGGTGGGGCTGCTGCTGTGC  
GGCTGCTGCGGCGCGCTGCGCGGCTCCGACGCGCGCGGTGCGCGGGAACCTTCGGGACGCCCTCTGGGGTAGCGCGC  
GAGCGCCCATCGCCCACTACTCGCGCTGCTCCTGGGACCTGCTGGAGTGCATGTAAGCGGCTAGGCGCGCTCT  
CCCGAGCACTCCCGTCTCGGTGCTCTCGGTGGACTTAAAGTCAACAGATTTATCTTTTATCAAGGCAAGTTCC  
ATGAGCGCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAAATGAATTTGGAGACCATTTCAAATCTGGGACCA  
GCTTCGGCAAAATATTACATTTCTCTCTTGGCTGGAAACAGGATTTGTTGAATCTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTTGAACCTTTGGACCTTAGCAGCAACAATATTTCAGAGCTCCAAATGCAATTTTCAGGCCCTACAG  
CTCAAAATATCTGTATCTCAACGACCAACGAGTACATCAATGGAACCTGGGATTTTGAACAATTTGGCCAAACACA  
CTCCTTGTGTTAAAGCTGAACGGAACCGAATCTCAGCTATCCACCCAAAGATGTTTAAACTGCCCAACTGCAAC  
CATCTCGAATTTGAACCGAAACAGATTTAAAAATGTAGATGGACTGACATTTCCAAGGCTTGGTGCTCTGAAGTCT  
CTGAAATGCAAGAAATGGAGTAAAGAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAATTTTGG  
CAGCTGGACCAATAACAACCTAAACAGAGATTACCAAGGCTGGCTTTACGGCTTGTGATGCTGCAGGAACCTTAT  
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCTGCGGAGTTCTGCGCAAGCTCAGTGAGCTGGACCTA  
ACTTTCAATCACTTATCAAGTTAGATGATTCAAGCTTCTTGGCTTAAAGCTTACTAAATACATGCACTTGGG  
AACAACAGAGTCACTGATCAATTTGCTGATGTTGCTTCCGGGGCTTTCAGTTTAAAGCTTTGGATCTGAAGAAC  
AATGAATTTTCTCGATATTGAAGACATGAATGGTGCTTCTCTGGGCTTGAACAACGAGGCGAGTACTACT  
CAAGAAATCGGATCGGTCTTATTACTAAAAAGCCTTCACTGGTTTGGATGCAATTTGGGACATCTAGACCTGAGT  
GACGAAACGAATCTGCTTTTCAAGGCAATGCAATTTTCAAAATGAAGAACTGCAACAAATGCAATTTAAATACA  
CTAAGCCTTTTGGTGCACTTGGCACTTAAATGGCTCCCAAGTGGGTGGCGGAAACAACTTTTCAGAGCTTGTGA  
ATGATGCAATTTGGCCATCTCTCAGCTGCTAAGGAGAAAGCACTTTTCTGCTTAGCCAGATGGCTTTTGTGT  
GATGATTTTCCCAACCCAGATCAGGCTCAGCAGAAACACAGTCGCGCAATAAAGGTTTCCAATTTGAGTTTC  
ATCTGCTCAGCTGCGCAGCAGCATGATTTCCCAATGACTTTTCTTGGAAAAAGACAATGAACCTCTGATGAT  
GCTGAAATGGAAATATTGACACACTCTCGGGCCCAAGGTGGAGGATATACCAACCACTCTTCGGCTG  
CGGAGGTGGAATTTGGCACTGAGGGGAAATATCAGTGTGTCATCTCCAACTCACTTTGGTTCATGCTACTCTGTC  
AAAGCAGAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCACTGATGATCACCATCCGCTGCGGGC  
ATGGCAGCTTGGATGTGCTGCTGTTGGGCGCCAGCAGCCCAAGATAGCCTGGCAGGAAGTTGGGGCAACAGAC  
TTCCAGCTGCACGGGAGACGCATGATGTGATGCCGAGGATGACGTGTTCTTATCGTGGATGTGAAGATA  
GAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAAGTATTTACGCAATGCACTCTGACTGTC  
CTAGAAACACCATCATTTTTCGGCCACTGTTGGACCGAATCTGAACCAAGGAGAAACAGCCGTCCTACAGTGC  
ATTTGCTGGAGAAAGCCCTCCCTCAAACTGAATGAGACCAAGATGATAGCCCAATTTGGTGTAAACCGAGAGGCAC  
TTTTTTGAGCAGCGCAATCAGCTTTCGATTATTGTTGGAATCAGATGTCAAGTATGCTGGGAAATCAATGTGAG  
ATGCTAAACACCTTTGCACTGAGAGAGGAAACGTGCGCTCAGTGTGATGCCCACTCCAACTCGCACTCCCT  
CAGATGACAGCCCATCGTTAGACGATGACGGATGGGCCACTGTTGGTGTGCTGATAGCCGTTGCTGTG  
GTGTTGGGCACTCACTCGTGTGGTGTGTCATCATATCAACAAGGCGGAGGAATGAAGATTTGACGATTAACC  
AACAACAGATGAGACCACTGCTTCCAGCAGATATTCCTAGTTATTGTCATCTCAGGGAACCTTAGCTGACAGGCA  
GATGGTACGTGCTTTCAGAAAGTGAAGGCCACCAAGCTTTGTCACTCTTCAGGTGCTGGATTTTCTTACCA  
CAACATGACAGTGTGGGACTTGCATATTGACAATAGCAGTGAAGCTGATGGGAAGCTGCCAGACATCTGTTCT  
CTTTGCTCGTTTGGGATCCACAGGCGCTATGATTTGAAGGGAATGTGATGCGCTCAGATCCTTTTGAACACA  
TATCATACAGGTTCAGCTCTGCACCAAGAACAGTTTTAAAGGCACTATGAGCCAGTATGACATAAAGAAAG  
GAGTGTACCCATGTTCTCATCTTTCAGAAAGATCTCGCAACGGAGCTTCAGTAAATATATCGTGGCTTCACAT  
GTGAGGAAGCTACTTTAACAATGATTACTCTCAATAAGGACCTGGAATGAAAAATCTGTGCTCTAACAAGTCT  
TCTTTAGATTTTATGCAAAATCAGAGCGAGCGTCTGGTGTGCTCAGTAAATTTTTCATGGGTACCTTTGGAACAA  
GCTCTCAGGAGACCTCAGCTAGATGCTTATTCAGCTTTGGAAGCTGATGAGTTCAGCAGCAAGACCTTTTAT  
TTGAAGGCTCATTTCTCCCACTTTGGACTCTGGGTGAGAGGAAGTGGGAAGAAAGCAAGACTTTTTCAGGAA  
GAAATACATATTTGATCTTTTAAACAGACTTTTAAAGAACTACAGGACTCCAAATTTTTCAGTCTTATGACTGTGAC  
ACATAGACTGAATGAGACCAAGGAAAGCTTAACTACTACTCTCAAGTGAACCTTTTATTTAAAGAGAGAGAT  
CTTATGTTTTTTTAAATGGAGTTTGAATTTTAAAGGATAAAATGCTTATTTATACAGATGAACCAAAATATAC  
AAAAAGTTTATGAAATTTTATCTGGGAATGATGCTCATTAAGAAATACCTTTTAAACTATTTTAACTTTG  
TTTTTAAATAAAGATCTTACGTAATTAATGATATAAATCATGATTTTATGATTTTATTAATGCCAGT  
TTTCTTTTATGGAATGAGTTACTTAAAGCATTTTAAATTAATACCTGCTTGTACCATTTTAAATGAGAGTT  
ACTTCATTTATTTTGCACATTTATTTTAAATAAATGTTCAATTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

## FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGLDLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSPANIT  
LLSLAGNRIVETILPEHLKEFQSLLETLDLSSNNISELQTAFAPALQKLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNISAIPPKMFKLPLQLQHLELNRNKIKNVDDLGLTFQGLGALKSLKMQR  
NGVTKLMDGAFWGLSNMEILQLDHNNTLITKGWLYGLLMLQELHLSQNAINRISPDWAEFC  
QKLSLELDLTFNHLRLDDSSFLGLSLNLTLLHIGNNRVSYIADCAFRGLSSSLKTLDLKNNIS  
WTIEDMNGAFSGLDKLRLLILQGNRIRISITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQQLHLNLTSSLLCDQLKWLPOWVAENNFQSFVNASCAPQLLKGRSIFAVSPDGFVCDFF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDKNELLHDAEMENYAHRAQGGG  
VMEYTTILRLREVEFASGKYQCVISNHFQSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHAPAOIAWQKDGTDFFAARERRMHVMPEDDVFFIVDVKIEDIGVYSTAQNISA  
GSISANATLTVLETPSFRLPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDSDPLVVTERHF  
FAAGNQLLIIVDSVDSDAGKYTCMSNTLGTGERGNVRLSVIPTPTCDSPQMTAPSLDDDDGWA  
TVGVVIAVVCVGTSLVWVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLDADQ  
DGVVSSSGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY  
LKGNVYSGDPFETYHTGCSPPDRPTVLMHDHYEPSYIKKCECPCSHSPSESCERSFNSISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFFKALRRPHLDAYS  
SFGQPSDCQPRAFYLLKAHSSFDLDSGSEEDGKERTDFQENHICTFKQTLNRYRTPNFQSYDLDT

### Signal sequence:

amino acids 1-27

### Transmembrane domain:

amino acids 808-828

### N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

### Glycosaminoglycan attachment site.

amino acids 886-890

### Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

### Tyrosine kinase phosphorylation site.

amino acids 667-675

### N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

### Leucine zipper pattern.

amino acids 58-80, 65-87

## FIGURE 107

CAAAACTTGCCTCGCGGAGAGCGCCAGCTTGACTTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC  
 TGGGGAGCGCGTTCGCGCTGTGGGCGCGCGCTCGGGCGCGGGGCGCAGCGAGGAAGGGAAGCTGTGGTCTGCC  
 CTGCTCCACGAGGGCGCACTGTGTGAACGGGAGAGCCCTGGGTGGTCCCTGCTTCCTCTCTTTATATA  
 GAAACCTTCCACACTGGGAAGGCGAGCGCGAGGCGAGGGCTCATGGTGAAGCAAGGAGGCGCGCTGATCTGCAG  
 GCGCAAGCATCTCCAGTTTACAGATTTTACAGATAACAAATGGAAGGCGAGGAGGCGAGAAACAGCTCGCTTGGT  
 TCCATCAGCCCTGGCGCCAGCGCGCATCTGACTCGGCACCCCTGCAAGGCACCATGGCCAGAGCCGGGTGGCTGC  
 TGCTCTGCTGCTGCTCGCGCCACAGCTGCACCTGGGACCTGTGCTTGCGGTGAGGGCCCCAGGATTTGGCGGAA  
 CTGGCGGGCCACAGCTTGAGCCCGGAGAGAACGAATTTGCGGAGGAGGAGCGCGGTGCTGTTACTTGAGCCCTGAGG  
 AGCCCGGGCTTGGCCAGCGCGGTGAGCTGCCCGGAGACTGTGCTGTTCCAGGAGGGCGCTCGTGAATGTG  
 GCGGTATTGACTTGCCTGAGTTCCCGGGGGACCTGCCGTGAGCACACCAACACCTATCTCTGCGAAGCAACACAGC  
 TGGAAAGAGATACCTCTGAGGAGCTTCCCGGCTGCACCGGCTGGAGACACTGAACTGCGAAGCAACACCACTGA  
 CTTCCCGAGGGCTCCAGAGAAAGGCGTTTGAAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAAATAACAAAGC  
 TGACCTTGGCACCCCGCTTCTGCCAAACGCCCTGATCAGTGTGGAATTTGCTGCCAATCTCTCACCAGATCT  
 ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACTGTCACAAACAACAGCTGGCAGAGCGCGGGC  
 TGCCGGAACAACATGTTCAACGGCTCCAGCAACGCTCGAGGTCTCATCTGTCCAGCAACTTCTCGCGCACGTG  
 CCAAGCACTCGCGCTGCCCTGTACAAGCTGCACCTCAAGAACAAACAGCTGGAGAGATCCCCCGGGCGCT  
 TCAGCGAGCTGAGCAGCTTGCAGGCTATACCTGCAGAACCACTACCTGACTGACGAGGGCTTGGACAAACGAGA  
 CCTTCTGGAAGCTCTCCAGCTTGAAGTACTGGATCTGTCCAGCAACCACTGTCTCGGGTCCAGCTGGCGTGC  
 CGCGCAGCTGGTGTCTGCTGCTGCTGCACTTGGAGAAGAACGCCATCCGAGCGTGGAGCGGAATGTGCTGACCCCATCC  
 CGAGCTGGAGTACTGCTGCTGCTGCACTGCACAGCAACAGCTCGGGGAGCAGGGCATCCACCCACTGCGCTTCCAGGGCC  
 TCAAGCGGTGACACAGGTCACCTGTACAACAACCGCTGGAGCGGCTGCCAGTGGCTGCTTCCGCGGCTGTG  
 GCACCTCATGATCTCTGCACACCAAGATCAAGGCATTTGGCGGAGAACTTTGCCACCACTACTTCTCTSGAGG  
 AGCTCAACCTCAGTACAACCACTCACAGGCCACAGGTGCACCGCGAGCGCTTCCGCAAGCTGCGCTGTCTG  
 GCTCGCTGAGCTGTGCGGCAACCGGCTGCACACGCTGCCACTGGGCTGCTTCAAAATGCTCATGTGCTGAAG  
 TCAAGGCAATGAGCTGTGCGGCGCTTGGCAGCAGGGGCGTGGCGGCGATGGCTGAGCTGTGACTCTCA  
 CCAGCAACCGACTCGCGAGCGGCTTGGGCCCCGCTGCTTGGGTGAGCTCGCCCATCTGAGCTGCTGGGCA  
 TCGCCGGGAATCAGCTCAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACCTGCGAAGCAACA  
 AGATTAGTGGTGGTCCCGCCCAATGCTTTCGACTTCCAGCCCAACCTCAAGGGCATCTTTCTCAGGTTTAAACAGC  
 TGGCTGTGGGCTCCGTGCTGGAAGTGCCTTCCGAGGCTGAAGCACTGCGAGGTCTTGGACATTGGAAGGCAACT  
 TAGAGTTTGTGACATTTCGAAGACCGTGGCGCTTGGGAGGAAAGGAGGAGGAGGAAGAGGAGGAGGAGG  
 AGGAAGAGGAAACAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCGGACTCTTTTCTGC  
 AGCACAGCTGTGTGCTGTGAGCCCCCACTTGCCTGTCTACACAGACACCCAGCTGCAACATGAGGCA  
 TCCACATGACACGGGCTGACACAGTCTATATCCCCACCCCTTCCACGCGGTGTCCACGGCCAGACACATGC  
 ACACACATCACACCTCAAACACCCAGCTCAGCCAACACAACTACCTCCAAACCAACCAAGTCTCTGTACAC  
 CCCCCTACCGCTGCCACGCCCTCTGAATCATGCAAGGGAAGGCTGTGCCCTGCTGCTGGCACACACAGGCCCA  
 TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACACACACACATGCACAACTCATGTGGGAA  
 CAGCCCTCCAAAGCCTATGCCACAGACAGCTTGTGCCAGGCCAGAAATCAGCCATAGCAGCTCGCGCTGTGCCCT  
 GTCCATCTGCTCCGCTCCGTTCCCTGGAGAGACACAAGGATATCCATGCTCTGTGGCGAGGTGCTGTCCACCTCT  
 GGAATCAACAAAGCTGGCTTTTATTCTTTCCCATCTCTATGGGGAAGGAGCTTTCAGGACTGCTGGCTGGCC  
 TGGCCGCCCTGCTCCTCCAGGTGCTGGGCACTACTCTGCTAAGAGTCCCTCCCTGCGACGCGCTGGCAGGACA  
 CAGGCACTTTTCAATGGGCAAGCCAGTGGAGGAGGATGGGAGAGCCCTTGGGTGCTGCTGGGCGCTTGGG  
 CAGGATGAGGAGGATGGGGCTGGGCTGAGCCAGGAGGAGGACCCAGCTGCACTGAGGAGACCTTT  
 GTTCTTCAGGCTGTGGGGGAAGTTCCGGTGCCTTTATTTTATTTCTTTTCAAGGAAAAAATGATAAAAT  
 CTCAAAGCTGATTTTCTGTATAGAAAAATAATAAAAAAGCATATCCCTATCCCTGCAAAAAA

## **FIGURE 108**

MEGEEAEQPAWFHQPWPRGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPFVLAVRAPGFGRS  
GGHSLSPREENEFAEEEPVLVLSPPEPGPGPAAVSCPRDCACSQEGVDDCGGIDLREFPGDLP  
EHTNHLSLQNNQLEKIYPEELSRHLRLETNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK  
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFGSSNV  
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLHNS  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYF  
LEELNLSYNRITSQVHRDAFRKRLRLSLDLSGNRLHTLPPGLPRNVHLKVKRNELAAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEEETR

### **Signal sequence:**

amino acids 1-48

### **N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

### **N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

### **Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCTCGCCGCTGCTCCTCGGGAGCGGCAG  
CAGTAGCCCGGGCGGCGAGGGCTTGGGGTTCTCGAGACTCTCAGAGGGGGCGCTCCCATCGGGCGCCACACCC  
CAACCTGTTCTCGCGCGCCACTGCGCTGCGCCCCAGGACCCGCTGCCCAACATGGATTCTCTCGGCGCTGGT  
GCTGGTATCTCGCTTACTGTCAGGCGGGCCGCGGAGTTTCGACGGGAGGTGGCCAGGCAAAATAGTGTATCGAT  
TGGCCTATGTGCTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGAAGTGTCCAGCC  
TGTGTGCCAACACGATGCAAAATCGGTGAATGTATCGGGCCAAACAAAGTGCAAGTGTATCTCTGGTTATGTGG  
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCCCGCCCTGTAAAGCACAGGGTGCAATGAACACTTA  
CGGCAGCTACAAGTGCTACTGTCTCAACGGATATATGCTCATGCGGGATGGTTCCTGCTCAAGTGCCCTGACCTG  
CTCCATGGCAAACTGTGAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCCGGGCT  
GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTGATGAATGTGCTACAGGAAGAGCCCTCTGCCCCAGATT  
TAGGCAATGCTCAACACTTTTGGGAGCTACATCTGCAAGTGTCAATAAGGCTTCGATCTCATGTATATTGAGAGG  
CAAAATATCAATGTCAATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTGTCTCGATGTTATAA  
CGTACGTGGGTCTTACAAGTGCAAAATGTAAAGAAGGATACCGGGTGTATGGAAGTGTGTTGTATATCCCAA  
AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAAGGGAATGTTACCATTTTAAAGGGTGACACAGGAAA  
TAATAATTGGATTCTGTATGTTGGAAGTACTTGGTGGCTCCGAAGACACCATATATTCTCTCATCATTACC  
CAGGCCACTCTTAAAGCAACAAACAGACCTACACCAAAGCCAAACCAATTCCTACTCCACCACCACACACC  
CCTGCCAACAGAGCTCAGAACACCTCTACCACTCAACCCAGAAAGGCCAACACCGGACTGACAACTATAG  
ACCAGCTGCCAGTACACTCTCCAGGAGGGATTACAGTTGACAAACAGGGTACAGACAGCCCTCAGAAACCCAGAG  
AGATGTGTTCAAGTGTCTGGTACACAGTTGTAATTTTGACCATGGACTTGTGATGGATCAGGAGGAAGACAA  
TGACTTGAACCTGGGAACCAATCAGGAGCCAGCAGGTGGACAAATATCTGACAGTGTCCGAGCCAAAGCCCGAG  
GGAGAAAGCTGCAGCTTGTGCTACTCTCGGCCCGCTCATGCACTCAGGGAGCTGTGCTCTGTCACTCAGGCA  
CAAGGTGCAGGGGCTGCACCTTGGCACAATCCAGGTGTTTGTGAGAAACACAGGTGCCACGAGCAGCTCGCTGTG  
GGAGAAATGTGTGCCATGGCTGGAGGCAACACAGATCACCTTGCAGGGGCTGACATCAAGAGCGAATCAC  
AAGATGATTAAGGGTTGGAAAAAAGATATGATGGAAAAATTAAGGAACCTGGGATTATTGAGCTTGGAGAAG  
AGAGAGCTGAGGGCAACACCATTTGATGGTTTCAAGTATATGAAGGGTTGCCACAGAGGGGTGGCCAGCAGCTG  
TTCTCCACTATGACCTAAGATAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTTCTTGGCAGG  
GGCCATTGTTAGAATACTTCTATAAAAAAAGAGGTGTGAAATCTCAGTATCTCTCTCTCTTTTAAAAAATTAGA  
TAAAAAATTTGCTATTTAAGATGGTTAAAGATGTTCTTACCACAGGAAAGTAAACAAATTATAGAAATTTCCCAA  
AGATGTTTGTATCTCTAGTAGTATGCAAGTAAATCTTTAGAACATAAATAATTTGGACAAGGCTTAATTTAGG  
CATTTCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCCAAAATGCTGAGCTCACTGAAATA  
TCTCTCCTTATGGCAATCTAGCAGTATTAAAGAAAAAAGGAACATATTATTCCAAATGAGAGTATGATGGAC  
AGATATTTAGTATCTCAGTAATGCTTAGTGTGGCGGTGGTTTCAATGTTTCTTCATGGTAAAGGATAAGCC  
TTTCATTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTAAAGAGATCCTTCAAGGAACACAGTTTCAGAGAG  
ATTTTCACTCGGGTGCTTCTCTCTCTGCTGTGTGACAAGTTATCTTGGCTGTGAGAAAGAGTGCCCTGGCCC  
ACACCGGCAGACCTTCTCTCACCTCATCAGTATGATTCAAGTTCTCTTATCAATTGGACTCTCCAGGTTCCAC  
AGAACAGTAAATTTTTTTGAACAAATAGGTACAATAGAAGGCTCTCTGTCATTAACTGGTAAAGGAGCGGCTGG  
TAGGGGGAAAAATAATCATTAAGCCTTTGAGTAACGGCAGAATATATGGCTGATAGTCCATTTTAAATGGTTCAAT  
TCCTTTATGGTCATATAACTGACAGCTGAAGATGAAAGGGGAAAAATAAATGAAATTTTACTTTTCGATGCCAA  
TGATACATTGCACTAACTGATGGGAAGGATTATCCAAAGTACTGTATAAATCTGTTTATTATTAAATGGTTT  
CTAAATAAAAAATGTAGTGGTTTTCCAAATGGCTAATAAAAACAATTGTTTGAATAAAAAACACTGTAGTAAAT

## **FIGURE 110**

MDFLALVLVSSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCGWARQSWGQCQPVCPQ  
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCOYGCDDVVKQIRQCQPSGLHLAPDGRTCVDVDECATGRASCPRFRQC  
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKNGNTILKGD TGNNWIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN  
RVQTD PQPRGDFVSVLVHSCNFDHGLCGWIREKDNLDLHWEPIRDPAGGQYLTVSAAKAPGG  
KAARLVLPGLRLMHSGDLCLSFRRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHWGRQTQI  
TLRGADIKSESQR

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 273-277

### **Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

### **Tyrosine kinase phosphorylation site.**

amino acids 199-206

### **N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

### **Cell attachment sequence.**

amino acids 382-385

### **EGF-like domain cysteine pattern signature.**

amino acids 75-87

## FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTGCCCCCTTTAGATTGTGA  
AAATGTGGCTCAAGGTCCTCACAACCTTTCTCTTTCCTTTGCAACAGGTGCTTGTGTCGGGGCTGA  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCGGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA  
CACAAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAAATACC  
AACACAAGTTTACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCACTTCCT  
GATGAAGCAATTACATCTGTGAAGGTCAACATTGAGGAAATGGAACCTATCTGCCAGTCA  
GAAGATACAAGTCACGGTTGATGATCCTGTGCACAAGCCAGTGGTGCAGATTATCCTCCCT  
CTGGGGCTGTGGAGTATGTGGGGAAACATGACCCTGACATGCCATGTGGAAAGGGGGCACTCGG  
CTAGCTTACCAATGGTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC  
TCCCCAAAACAATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
GCCTGGTGAGGAACCTGTGCTAGTGAAATGGAAAGTGATATCATTATGCCATCATATATTAT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAAGTAGGGGAAGTGTTTACTGT  
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGCACAATACTACATATATCATTAAAGCATGGGCCTCGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC  
CGGCAGGCAAGATGAAACTCATTTCACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG  
CACAGAAAGGAAAATCATTGTCACTTTTAGCAAGTATAACTGGAATATCACTATTTTGGATT  
ATATCCATGTGTCTTCTCTTCCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAACATTTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTCACAGG  
ATTCCAAGCAGGTCTGTTCAGCCCTCTGATTGTGTATCGGGGCAAGATTGACACAGTACAGT  
GTATGAAGTTATTGACACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACCTTCATGG  
CTAAACAGTACATTGAGTGAAATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAGT  
ATATTAATCTGGAATCAGTGAAGAAACACAGGACCAACACCTCTTACTCATTATTCCTTTACA  
TGCAGAAATAGAGGCATTTATGCAAAATGAACTGCAGGTTTTTCAGCATATACACAATGTCTT  
GTGCAACAGAAAAACATGTTGGGGAAATATTCTCAGTGGAGAGTCTGTTCTCATGTCTGACGG  
GGAGAACGAAAGTGACAGGGGTTTCTCTATAAGTTTGTATGAATAATCTCTPACAAACCTCA  
ATTAGTCTACTCTACACTTTCATATCATCAACACTGAGACTATCCTGTCTCACCTACAAA  
TGTGGAACCTTTACATTGTTTCGATTTTTCAGCAGACTTTGTTTTATTAATTTTATTTAGTG  
TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTGTTATTTGTACAA  
CAAAGTAATAAGGATGGTTGTGCAAAAACAAACTATGCCTTCTCTTTTTTTTCAATCACC  
AGTAGTATTTTTGAGAAGACTGTGAACACTTAAGGAAATGACTATTAAGTCTTATTTTTTA  
TTTTTTTCAAGGAAAGATGGATTCAAATAAATATTCTGTTTTTGGCTTTTAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNIVKVNIQNGTSLASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPFVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTM DYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPIRSVPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 341-359

### **N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

### **Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

### **Tyrosine kinase phosphorylation site.**

amino acids 272-280

### **N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



## FIGURE 113

GCAAGCGGCGAAATGCGCCCTCCGGGAGTCTTGCAGTTCCCCTGGCAGTCTGGTGTCTGTT  
GCTTTGGGGTGTCTCCCTGGACGCACGGGCGGCGGAGCAACGTTTCGCGTCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCGTGGTGCCTGTCT  
TGTCAAAATCTTCAACCGGAATGGGAAAAGTTTTGCTGAATGGGAGAAAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCCTC  
TTCTACTATTTTATCATTTGTAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAATCTTATAAGTGATAAAGAGTGGAAAGATATTGAGCCCGTTTCATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT  
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC  
AGATTGCCTTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTTCAAAAAAT  
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGCGGATGAAGAA  
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAACAAGACTTTCACAGAATGC  
CATAAGACAACGCTCTCTGGGTCCATCATTTGGCCACAGATAAATCTTAGTTAAATTTTATAG  
TTATCTTAATATTATGATTTTGATAAAAACAGAAGATTGATCATTTTGTGTGGTTTGAAGTG  
AACTGTGACTTTTTTGAATATTCAGGGTTCAGTCTAGATTGTCAATTAATGAAGAGTCTA  
CATTCAGAACAATAAAGCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATG  
GTTTAAATAGTTCTCTAATTTTGAAAAATCGTGCCAAAGCAATAAGATTATGATATTTGT  
TTAATAATAAAGCCTATTTCAAGTCTGAGTTTTGAAAAATTTACATTTCCCAAGTATTGCAAT  
TGAGGTATTTAAGAAGATTATTTTGAAGAAAAATTTCTCATTTGATATAATTTTCTCTG  
TTTCACTGTGTAAAAAAGAAGATATTTCCATAAATGGGAAGTTGGCCATTGTCTCAAG  
AAATGTGTATTTCAGTGACAAATTCGTGGTCTTTTAGAGGTATATCCAAAAATTTCTCTGT  
ATTTTATAGTTATGCAACTAATAAAAACACCTTACATTAATTAATTACAGTTTTCTACACA  
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTC  
CAACAAAAGTTGATTTTCTCTGTATTTTCTTACTTACTATGGGTACATTTTATTTTTT  
CAAAATGGATGATAATTTCTTGAAACATTTTTATGTTTTAGTAACAGTATTTTTTGT  
GTTTTCAAACTGAAGTTTACTGAGAGATCCATCAAAATGAACAATCTGTTGTAATTTAAAAAT  
TTGGCCACTTTTTTCAGATTTTACATCATTCCTGTCTGAACCTTCAACTTGAAATGTTTTTT  
TTTCTTTTTGGATGTGAAGGTGAACATTCTGATTTTTGTCTGATGTGAAAAAGCCTTGGTA  
TTTTTACATTTTGAAAAATTCAAAGAAGCTTAATATAAAAGTTTGCAATCTACTCAGGAAAAAG  
CATCTCTTGTATATGTCTTAAATGTATTTTGTCCCTCATATACAGAAAGTTCTAATTGAT  
TTTACAGTCTGTAATGCTTGATGTTTTAAAAATAATAACATTTTTATATTTTTTAAAGACAA  
ACTTCATATTATCTCTGTGTTCTTCTCTGACTGGTAATATTGTGTGGGATTTACAGGTA  
GTCAGTAGGATGGAACATTTTAGTGATATTTTACTCCTTAAAGAGCTAGAATACATAGTTTT  
CACCTTAAAGAAAGGGGAAAAATCATAAATACAATGAATCACTCAACCATACGTAGTAGAC  
AATTCTGTAATGTCCCTCTTCTTAGGCTCTGTGTGCTGTGTAATCCATTAGATTTACAG  
TATCGTAATATAACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCATT  
AAAGAGTTTGGATGTGTAACCTGTGATGCTCTAGAAAAATATCTAAGCACAAAATAAACCT  
TTCTAACCACTTCATTAAAGCTGAAAAA

## **FIGURE 114**

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKWKSIIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPKRRRPQYPYPYPSKLLSESAQPLKKVEEQEADEEDVSE  
EEAESKEGTNKDFPQNAIQRSLGPSLATDKS

### **Signal sequence:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 182-201

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

### **Tyrosine kinase phosphorylation site.**

amino acids 107-115

### **N-myristoylation site.**

amino acids 20-26, 192-198

### **Amidation site.**

amino acids 25-29

## **FIGURE 115**

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCTGTTAACTAATTCAACAAACGGGACCCTT  
 CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGCGGGATTGGAAGAGCGGG  
 AAGGTCCTGGCCCCAGAGCAGTGTGACACTTCCCTCTGTGACC**ATG**AAACTCTGGGTGTCTGC  
 ATTGCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCTTACCTCTATTG  
 GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC  
 CTTTGGAGGAAGCCAAAGCTTTTCCAAGATTAAGAGCTGGGCCAAACAAATGGAAGCCTTGAC  
 TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCTCAAACTGG  
 TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTCTGAGGACTCAGCTGCA  
 GGTTTTATCGCAACCTCTCTGTGCAGCGGCAGTTCTTCCCACTGATGAGGACGAGATAGG  
 AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA  
 GAGGGGAACCTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG  
 GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT  
 AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA  
 GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCTGCTC  
 TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA  
 GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA  
 TCTATGAGAGGCTGTGGACTACCTGCGCTGAGAGGGATGTTTACGAGAGCCTTGTGCTGGG  
 GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCAACATGGCAA  
 CAGGGCCCCACAGCTGCTCATTTGCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA  
 TCGTCAGGTACTACGATGTCATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA  
 CCTAAACCTGCACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCTCTACTGTGCCAGCTA  
 CCGGTTTTCAAAGCTCTTGGCTAGAGGAAGATGATGACCTGTGTGGCCCGAGTAAATC  
 GTCGGATGCAGCATATCACAGGGTTAAACGTAAGACTGCAGAATTGTTACAGGTTGCAAAAT  
 TATGGATGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG  
 CCTCAAACAGAGGGGAATAGGTTAGCGACGTTTTCTTAACTACATGAGTGATGTAGAAGCTG  
 GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCCTAAGAAGGGTACAGCTGTG  
 TCTCGGTACAACCTCTTGGGAGCGGGGAAGGTGACTACCGAACAAGACATGTGCGCTGCC  
 TGTGCTTGTGGGTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT  
 TGAGACCTTGTGGATCAACAGAAGTTGAC**TGA**CATCCTTTTCTGTCTCTCCCTTCTCTGGTC  
 CTTTCAGCCATGTCAAAGTGACAGACACCTTTGTATGTTCCCTTGTATGTTCCATACAGGCT  
 GATTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
 GTGACTGAAGTCCAGCCCTTCCATTTCAGCTGTGCCATCCTTGCCCCCAAGCTAGGATCA  
 AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCCTTTGTACCTCAGGTGTT  
 TTAGGTGTGAGATGTTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTTTTAT  
 GGCATTTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDLVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAALKMRLQDTYRLDPGTISRGEPLGTTYQAMLSVDDCFGMGRSAYNEGDIYYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR  
YFEQLLEEREKTLTNQTEAELATPEGIYERPDYLPERDVYESLCRGEVGLTPPRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYVDVMSDEEIERIKEIAKPKLARATVRDPKTF  
VLTVASYRVSKSSWLEDDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDPS  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYR  
TRHAACPVLVGCKWVSNKWPFHERGQEFLRPCGSTEV

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,

346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## FIGURE 117

GCAGTATTGAGTTTACTTCTCTCTTTTGTGGAAGACAGACCATAATCCAGTGTGAGTGAAATTGATTGT  
 TTCATTATTACCGTTTGGCTGGGGGTTAGTTCGCACACTTCACAGTTGAAGAGCAGGCAAGAGGATGTGGA  
 AGACAGGACAATCTCTTAGGGGATGCTGGTCTGGAAGCCAGCGGGCTTGCTGTCTTTGGCCTCATTGACCC  
 CAGGTTCTCTGGTTAAAACTGAAAGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCC  
 CCTGGGGCACCCAGCTGGCAGGGCCTACCACTATGCGACTGAGCTCCCTGTGGCTGTGCTGGGGCAGCGCTTC  
 CCTCATCTTAGGGCTGTCTCTGGGGTGCAGCCTGAGCCTCTGCGGGTTTCTGGATCCAGGGGGAGGGAGAAG  
 ATCCTGTGTGAGGGCTGTAGGGAGCGAGGAGGCCACAGAATCCAGATTTCGAGAGCTCGGCTAGACCAAAATG  
 ATGAAGACTCAAAACCCCGGATTGTCCCCTACTACAGGGACCCCAACAGCCCTACAAGAAGGTGTCTCAGGACTC  
 GGTACATCCAGACAGAGCTGGGCTCCCGTGGCGGTTGCTGGTGGCTGTCTGACCTCCCGAGCTACACAGTCCA  
 CTTTGGCGGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCTCGGTTACTTACTTCTCTGGGAGCGGGGGG  
 CCGGGCTCCAGCAGGAGTGCAGTGGTGTCTCATGGGATGAGCGGCCCGCTGGCTCATGTGAGAGCCCTGC  
 GCCACTCTCACACACACTTTGGGGCCGACTACGACTGGTCTTCTCATCATGCAGGATGACACATATGTGCAGGCC  
 CCGCCTGGCAGCCCTTGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGCAGAGGAGTTCAATTG  
 GCGCAGCGAGCAGGCCCGGTACTGTCTAGGGGCTTTGGCTACCTGTTGTGACGGAGTCTCTGTCTCTGTCTGC  
 GGCACTCTGATGAGCTCCGAGGAGACATTCTAGTGCCCTCTGACGAGTGGCTTGACGCTGCTCATTTG  
 ACTCTCTGGGCTCGCTGTGTCTCACAGCACAGGGGCCAGCAGTATCGCTCATTGAACTGGCCAAAATAGGG  
 ACCTTGAGAAGGAGGAGCTCGGCTTCTGAGTGCTTCGCCGTGACCCCTGTCTCCGAAGGTACCCCTCATGT  
 ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAATATAGAACACTGCAGGCTCAGA  
 TCGGAACCTCAGCGTGTGACCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTCA  
 CACCACTCTCTCGCTTTGAGGTGTGGGCTGGGACTACTTCACAGAGCAGCACCTTCTCTGTGCAAGTGGG  
 CTCCCAAGTGCCACTACAGGGGGCTAGCAGGGCGGACGTGGTGATGCTTGGAGACTGCCTCTGGAGCAGCTCA  
 ATCGCGCTATCAGCCCGCTCGCTTCCAGAAGCAGCGACTGTCTCAACGGCTATCGGCGCTTCGACCCAGCATC  
 GGGGATGAGTACACCTGGACCTGTCTTGGAAATGTGTGACACAGCGTGGGCACCGCGGGCCCTGGCTCGCA  
 GGGTCAGCTCTGCTGGGCCACTGAGCGGGTGAATCTTACTATGCCCTATGTCTCATGAGGCCACCCGAGTGC  
 AGCTGTGTCTGCCACTCTGTGTGGCTGAAGCTGTGTCAGCCCCGGCTTCTCTCGAGCGCTTTGAGCCAATGTCC  
 TGGAGCCACGAGAACATGCATTGCTCACCTGTTGCTGGTCTACGGGCCACGAGAAGGTGGCCCTGGAGCTCCAG  
 ACCATTTCTTGGGTGAAGGCTGCAGAGCGGAGTTAGAGCGACGCTACCTGGGACGAGGCTGGCTGGCTCG  
 CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCTCTGGGACACTCTCT  
 TCTTCTTACACCGTGTGGAAGGCGCTGGGCCCGAAGTCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT  
 GGCAGGCTCTTTCCAGTCCATTTCAGGAGTTCAATCTGCTGCTGTGACCAAGAGATCACCCCGAGGGCCCC  
 CGGGGCTGGCCCTGACCCCCCTCCCTCCTGTGCTGACCCCTCCGGGGGGCTCTATAGGGGGGAGATTTG  
 ACCGGCAGGCTTCTGCGGAGGCTGCTTCTACAAACGCTGACTACCTGGCGGGCCGAGCCCGCTGGCAGGTGAAC  
 TGGCAGGCGCAGGAAGGAGGAAGCCCTGGAGGGGCTGGAGGTGATGATGTTTCTCTCGGTTCTCAGGGCTCC  
 ACCTCTTTCGGGCCGTAGAGCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCACGGCTCAGTGAAG  
 AACTCTACACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGGCGTGCACGCTGGCTATGGCTCTCTTTG  
 AGCAGGAGCAGCCCAATAGCACTTAGCCCGCTGGGGCCCTAACCTCATTACCTTCTTGTCTGCTCAGCC  
 CCAGGAAGGGCAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAATGTTATTAA  
 ACATGTCTCTTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQEGEGDPCVEAVGERGGPQNPDSSRARLD  
QSDPDFKPRIVPYRDPNPKPYKKVLRTRYIQTELGSRRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVS HGDERP A WLMSETLRHLHTHFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG  
DILSARPDWEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLT VLTPEGEAGLSWPVGLPAPFTPHSRFEV  
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRFQKQRLNGYR  
RFDPARMEYTLDDLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVPLLL  
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDFFLGVKAAAAELERRYPG  
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLT V WTRPGPEVLNRCRMNAISGWQAFPP  
VHFQEFNPALSPQRSPPGPPGAGDPSPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLA  
RARLAGELAGQEEEEALEGLEVMVDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRAQLAMALFEQE QANST

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 489-507

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250

## FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCTGTCCCCAAGCC  
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG  
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAAATTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTGAGTATACTGTATTATCCTTGTAACC  
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACTGTGACAAAGCAG  
AGTTCTTCAGTTCTGAAAAATGTTAAAGTGTTCAGTCAATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACATG  
GTTCTTCTTGCACGCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTTAA  
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT  
CAATATCCCAGAAAAGTGTCCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC  
CAACCAGGTAGTAGAAGGCTGTTGTTGAGATATGGCTGTTACTTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGATGTATGGGTATACCGCCTTAGGGCATTGGGCATATTTTCAAT  
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACACATATCCAA  
TACAGCTGTATGTTTCTTTTCTTTTCTAATTGGTGGCACTGGTATAACCACACATTAAG  
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTCTTTTAAACACATGAACATTGTAAATG  
TGTTGGAAGAAGTGTTTAAAGAATAAATTTGCAAATAAACTATTAATAAATATATAT  
GTGATAAATTTAAATTTATGAACATTAGAAATCTGTGGGCACATATTTTGTGATGGTT  
AAAAAATTTTAAAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT  
AAGCCTCCCCAAGTTCCAATGGATTGCGTTCTCAAAATGTACAATAAGCAACTAAAGAAA  
ATTAAAGTGAAAGTTGAAAAAT

## **FIGURE 120**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISED  
LSKSRVYCIILVKPKDVSLWAAVKETWTKHCDKAFFSSENVKVFESINMDTNDMWLM  
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLKKDPSQPFYLGHTIKSGDLEYV  
IVLSVESMKRLNSLLNIPEKCPEQGGMWIKISEDKQLAVCLKYAGVFAENAEDADGK  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFND  
ALVFLP  
P  
NGSDND

### **Signal sequence:**

amino acids 1-33

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250



Figure 1 illustrates the steps of the proposed algorithm for finding a minimum spanning tree. The diagrams show a graph with 6 nodes and 10 edges, with edges being added or removed to build the tree. The steps are labeled 1 through 12.

[illegible]

## **FIGURE 122**

MNSSKSSETQCTERGCFSQMLWTVAGIPILFLSACFITRCVVTRIFQTCDEKKFQLPEN  
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLED CATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

### **Signal sequence:**

amino acids 1-42

### **N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

### **N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCTCAGCAACCCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGGCTCGGCTGCGCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCGCTGATGAGGGCTGTAAATC  
TCAAACTCAGCAATCGAACCCAGCTGGTACAGGAATTTGAAAGTGTGGAACCTGCTTGCATCATTTACGAGATTGCG  
AGACAAGTGACCCACAGGATCGAGTGGGAAGAAATTCAGATGAAACAAACCATATGTGTTTGTGACACACAAA  
TTCAGGGAGCTTTGGCGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAAATGTGACACCGGAGAG  
ACTCAGCCCTTTATCGCTGTAGGCTGCTGCTCGAAATGACCGCAAGGAAATGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAAGCCAGTGACCCCTGTCTGTAGAGTGGCGAAGGCTGACAGTAGGCAAGATGGCAACCATGCG  
ACTGCCAGGAGATGAGGGCCACCCCGGCTCCTACACAGCTGGTATCGCAATGATGTACCATGCCCCAGGATT  
CCAGAGCCAAATCCAGATTTCGCAATTTCTTTCACCTTAAACTCTGAAACAGGCACTTTGGTGTCTCACTGCTG  
TTCACAAGGACGACTCTGGGCGACTACTGCTGCTTCCAATGACCGAGGCTCAGCCAGGTTGTAGGCGCAGG  
AGATGGAGTGTATGACCTGAACATTGGCGAAATTAATTGGGGGGTCTGGTGTCTGCTGTACTGGCCCTGA  
TCCAGTTGGGCTATCTGCTGTGCATACAGAGTGGCTACTTCACTCAACAAATAACAGGATGGAGAAAGTTACAAAG  
ACCCAGGGAACCCAGATGGAGTTAACTACATCCGCACTGACAGGAGGGCGACTCAGACACAAGTCATCGTTTG  
TGATCTGACGCCCGGCTGTGGCTGAGAGCGCACAGAGCCGACGTCACATACCTCTGCTAGAAATCTCTGTCAA  
GGCAGCGAGAGCTGATGCATCTCGACAGAGCTAGACACTCATTCAGAAGCTTTTCGTTTGGGCCAAAGTTGACCA  
CTACTCTTCTACTCTAACAGCCACATGAATAGAAGAAATTTCTCAAGATGGACCAGCCGTAATAATAACCAAA  
GGAAGCGAAATCGGTGCGTTCACTGAGTTGGGTTCTTAATCTGTTTCTGGCTGATTCCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTTCTCATCGTAAACCCCGCTGCTGGGCCCTGTGAAGCGAGCATGTTCAACCATGGTGGT  
CAGCAGCCACGACAGCCATGTGAGATGGCGAGGTGGCTGGACAGCAGCAGCGCATCCCGCGCGGAACCCA  
GAAAGAGCTCTTACACAGCAGCTTACTTTCATCGGCCACAGACACACCCGACGTTTCTCTTAAAGGCTCTGC  
TGATCGGTGTGCACTGTGCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG  
GTAATTTGGTTGCTGGAAGAGGATCTTGCCTGAGGAACCTGCTTGTCCAACAGGTTGTGAGGTTTAAAGAAA  
ACCTCTGCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTATAAAATTT  
TACATCTAAATTTTGTCAAGGATGATTTTGATTATTGAAAGAAATTTCTATTAAACCTGTAATATATATTGT  
CATACAATGTTAAATAACCTATTTTAAAAAGATTCAACTTAAGGTAGAAGTCCAAGCTACTAGTGTAAAT  
TGGAAATATCAATAATTAAAGATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCCCTTTCT  
CACACAAGTTTATGCTTTTTCACAAGGGAACCTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATTCAGTTTAAGCAATGTTGAAATCAGTTTGATCTCTTCAAAAGAACTCTCAGGTTAGCTTTGAAT  
GCCTCTTCTGAGTAGCTAGGACAGTCTGTACCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG  
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTGCTGCTGCTGCCAGGAGGCCCT  
GCCATCCTTGGGCCCTGGCAGTGGCTGTGCCAGTGAGCTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGAACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAAACAGACCTCT  
TTTTGGTTATGGATGGCTCAAAAATAGGGCCCCCAATGCTATTTTTTTTTTAAAGTTTGTGTTAAATATTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAAATACATTTTAAAAAGAAATGGAT  
CCCATGTTCTCTTTGCCCATAGGAAGCAACCCAGCGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT  
GGATGGCGGCCAGTCCAGCTTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCCCTGGCGGGGAGGAAG  
TGAACCGCTGAATCAAAAGCAGTTTCTAATTTGACTTTAAATTTTCTCGCGGGAGCACTGCTCCCAAT  
TGTGGGGGGATAGCAACTCACTCAGAAGCTGTGTTCTTCAAGACAGGTGATGCTTCAAGCTCAGCTGAGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTCTTAAAGCAAGGAGTGTCTGAGAAGGAGCACTCCACTGTGTGCTGTGA  
GAATGCTCTCACTACTCACTTCTTTTCAGCTCCAGTGTCTTGGGTTTTTATGCTTTGACAGCTCTTTTTTT  
AATTGCATACATGAGACTGTGTGACTTTTTTTTAGTTATGTGAAACACTTTGCGCCAGGCGCCCTGGCAGAGGCA  
GGAATGTCTAAGGCTGAGTGGCTGAGTGTCCCTGGTCTGCTGCTAGTGCATCTGAGCTCTAGCATGCAAGTCT  
CCTCCATGTTCCGACCTTGTGTAGAGAGGATGGCTCCCCACCTCAGCGTGGGATTCACGCTCCAGCTCTCT  
TCTTGTGTGTATGATGATGAGGTAGCTTTATTTGCCCCCTCTCTTATATACCTTAAACCTCTACACTAGTSCCA  
TGGGAACCGAGTCTGAAAGATGAGAGAAAGTGAAGTAGAGTCTGGGAAGTAGTGTGCTTAACTGAGACTAGA  
CGGAAAGGAATACTCGTGTATTTAAGATATGAATGTGACTCAAGCTCGAGGCCGATAGAGGCTGTGATTTCT  
GCCTTTGATGGATGTTGCTGTACACAGATGCTACAGACTGTGACTACACACCGGTAAATTTGGCATTTGTTTAAAC  
CTCATTTATAAAGCTTCAAAAAACCA

## **FIGURE 124**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTFVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSCLKIWNVTRRDSALYRCEVVARNDR
EIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWRNDVPLPTDSRA
NPRFRNSSFHLNSETGLTVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVEVDLNIIGGI
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNIIRTDEEGDFRHKSSFVI
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-30

#### **Transmembrane domain:**

amino acids 243-263

#### **N-glycosylation sites.**

amino acids 104-107, 192-195

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

#### **Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

#### **Tyrosine kinase phosphorylation site.**

amino acids 69-77

#### **N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267